

Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His
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 Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val Ile Ala Val Phe Asp
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 Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu Thr Leu Pro Ala Val
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 His Ser Ala Lys Arg Val Trp Leu Leu Val Ser Gly Ala Glu Lys Ala
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 gag gca gct gcg gcg atc gtc aac ggt gag cct gct gtt gag tgg cct 739
 Glu Ala Ala Ala Ile Val Asn Gly Glu Pro Ala Val Glu Trp Pro
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 gct gct gga gct acc gga tct gag gaa acg gta ttg ttc ttg gct gat 787
 Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val Leu Phe Leu Ala Asp
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Met Ser Lys Thr Ile 5																
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Ile Val Arg Thr Glu Ile Glu Ile Pro Gly His Pro Thr Ala Ile His 20																
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069370-10

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 Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr
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 Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu
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 Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val Gly Asp Asn Val His
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gga cct gag tac tac cac cgc cag ctt ggc gat atc ctg tac ttc tcc 1747
 Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser
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Pro	Ala	Gly	Val	Pro	Thr	Lys	Asp	Met	Trp	Glu	Tyr	Gln	Lys	Asp	His
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Leu	Gly	Tyr	Asp	Val	Lys	Ala	Phe	Thr	Tyr	His	Asp	Ala	Pro	Arg	Arg
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Ala	His	Ser	Ile	Ala	Ala	Gln	Gly	Gly	Val	Asn	Ser	Ala	Arg	Gly	Lys
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Gln	Val	Ser	Arg	Thr	Tyr	Tyr	Thr	Arg	Gly	Gln	Thr	Gly	Gln	Gln	Leu
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 Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn
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 Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro
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 Ala Phe Gly Asn Leu Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser
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 Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile
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 Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly
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 Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser
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 Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg
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 Ala Gln Ala Arg Ile Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val
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 Gly Asp Asn Val His Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp
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 Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val
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His Leu Ser Glu Asp Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys
 625 630 635 640

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Lys

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 Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe
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ctg gag cgc cgc tac cca gca ttc ggt aac ctc gtc cca cgt gac gtt 144
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 Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn
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 Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile
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 Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu
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 Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala
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 225 230 235 240
 Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg
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 Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met
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Phe	Pro	Leu	Ala	Met	Ala	Thr	Arg	Lys	Val	Ala	Pro	Ala	Ile	Ala	Ala
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Val	Gly	Gln	Gln	Leu	Leu	Lys	Lys	Ala	Ala	Asp	Lys	Val	Leu	Arg	Thr
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Met Lys Leu Thr Leu																5
gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc																163
Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr																20
gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt																211
Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu																35
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Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala																50
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Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu																65
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Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala																85
cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca																403
Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro																100
ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc																451
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Thr	Cys	Gly	Leu	Leu	Val	Asn	Gly	Arg	Pro	His	Gly	Ala	Asp	Gln	Asn	
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Lys	Pro	Ala	Cys	Ala	Gln	Arg	Leu	Val	Ser	Tyr	Lys	Glu	Gly	Asp	Thr	
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Leu	Lys	Ile	Glu	Pro	Leu	Arg	Ser	Ala	Ala	Tyr	Pro	Val	Ile	Lys	Asp	
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 Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
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 Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
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 Met Thr Glu Gln Glu
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 Phe Arg Ile Glu His Asp Thr Met Gly Glu Val Lys Val Pro Ala Lys
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 gct ctg tgg cag gca cag acc cag cgc gct gtt gag aac ttc cct atc 211
 Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val Glu Asn Phe Pro Ile
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 tct ggt cgt ggt ctg gaa tcc gca cag atc cgc gca atg ggt ctg ctg 259
 Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg Ala Met Gly Leu Leu
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 aag gca gct tgt gcg cag gta aac aag gac tcc ggt gcg ctg gat gca 307
 Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser Gly Ala Leu Asp Ala
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Ala	Met	Gly	Leu	Leu	Lys	Ala	Ala	Cys	Ala	Gln	Val	Asn	Lys	Asp	Ser	
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Gly	Ala	Leu	Asp	Ala	Glu	Lys	Ala	Asp	Ala	Ile	Ile	Ala	Ala	Gly	Lys	
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Gly Ala Leu Asp Ala Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys
65 70 75 80

	405						410						415					
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Pro	Glu	Thr	Trp	Ala	Ile	Thr	Ser	Glu	Gly	Ala	Pro	Thr	Thr	Asp	Pro		
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Ala	Glu	Ala	Ile	Asn	Gly	Val	Val	Leu	Pro	Met	Ala	Gly	His	Lys	Gly		
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Tyr	Ala	Ile	Ser	Phe	Met	Met	Asp	Val	Leu	Ser	Gly	Val	Leu	Thr	Gly		
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Ser	Gln	His	Ser	Thr	Lys	Val	His	Gly	Pro	Tyr	Asp	Pro	Thr	Pro	Pro		
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ggg	gga	gct	ggc	cac	ttg	ttc	atc	gcg	ttg	gat	gtt	gca	gcg	ttt	cg	931	
Gly	Gly	Ala	Gly	His	Leu	Phe	Ile	Ala	Leu	Asp	Val	Ala	Ala	Phe	Arg		
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gat	cca	caa	gat	ttc	gat	gac	gca	ctc	agc	gat	ctg	gtt	ggg	gaa	gtt	979	
Asp	Pro	Gln	Asp	Phe	Asp	Asp	Ala	Leu	Ser	Asp	Leu	Val	Gly	Glu	Val		
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Val	Leu	Arg	Leu	Pro	Trp	Tyr	Val	Arg	Arg	Leu	His	Ser	Gly	Ala	Met
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Pro	Trp	Ser	Ile	Ala	Ala	Pro	Phe	Gly	Glu	Thr	Ala	Thr	Val	Val	Asp
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Ile	Ala	Asn	Thr	Ala	Val	Ala	Arg	Gly	Lys	Ile	Tyr	His	Ala	Arg	Gln
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Val	Ala	Ala	Phe	Arg	Asp	Pro	Gln	Asp	Phe	Asp	Asp	Ala	Leu	Ser	Asp
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Leu	Val	Gly	Glu	Val	Lys	Ser	Thr	Pro	Lys	Ala	Gln	Asn	Thr	Glu	Glu
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Ile Phe Tyr Pro Gly Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser
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Met Asn Ser Pro Gln
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Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly Ala Ala Gly Gln Ile
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Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu Val Phe Gly Thr
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gac acc cct gta gaa ctg aaa ctt ctg gag atc cct cag gct ctt ggc 259
Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile Pro Gln Ala Leu Gly
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Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser Ala Phe Pro Leu
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Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn Glu Ala Phe Asp Gly
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gct aat gcg gcg ttt ttg gtc ggt gcg aag cct cgc gga aaa ggc gaa 403
Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Lys Gly Glu
90 95 100

gag cgc gca gat ttg ctg gct aac aac ggc aag att ttc gga cct caa 451
Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys Ile Phe Gly Pro Gln
105 110 115

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Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile Arg Val Leu Val
120 125 130

gtt gga aac cca gcg aac acc aac gcg ttg att gct tca gct gcg gcc 547

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Pro	Gln 50	Ala	Leu	Gly	Gly	Ala 55	Glu	Gly	Val	Ala	Met 60	Glu	Leu	Leu	Asp
Ser 65	Ala	Phe	Pro	Leu	Leu 70	Arg	Asn	Ile	Thr	Ile 75	Thr	Ala	Asp	Ala	Asn 80
Glu	Ala	Phe	Asp	Gly 85	Ala	Asn	Ala	Ala	Phe 90	Leu	Val	Gly	Ala	Lys 95	Pro
Arg	Gly	Lys	Gly 100	Glu	Glu	Arg	Ala	Asp 105	Leu	Leu	Ala	Asn	Asn 110	Gly	Lys
Ile	Phe 115	Gly	Pro	Gln	Gly	Lys	Ala 120	Ile	Asn	Asp	Asn	Ala 125	Ala	Asp	Asp
Ile 130	Arg	Val	Leu	Val	Val	Gly 135	Asn	Pro	Ala	Asn	Thr 140	Asn	Ala	Leu	Ile
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Gly	Arg	Gly	Ser 180	Ala	Glu	Phe	Asn	Asn 185	Ile	Val	Val	Trp	Gly 190	Asn	His
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Pro 225	Arg	Val	Ala	Asn	Arg 230	Gly	Ala	Glu	Ile	Ile 235	Glu	Val	Arg	Gly	Lys 240
Ser	Ser	Ala	Ala	Ser 245	Ala	Ala	Ser	Ser	Ala 250	Ile	Asp	His	Met	Arg 255	Asp
Trp	Val	Gln	Gly 260	Thr	Glu	Ala	Trp	Ser 265	Ser	Ala	Ala	Ile	Pro 270	Ser	Thr
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Phe 305	Gln	Arg	Ala	Arg	Ile 310	Asp	Ala	Asn	Ala	Gln 315	Glu	Leu	Gln	Ala	Glu 320
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gcc		agt	ttc	gcg	gtg	ggc	ttt	gac	atc	ggc	ggc	acc	aac	atg	cga	gcc	163
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Gly		Leu	Val	Asp	Glu	Ser	Gly	Arg	Ile	Val	Thr	Ser	Leu	Ser	Ala	Pro	35
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Ser		Pro	Arg	Thr	Thr	Gln	Ala	Met	Glu	Gln	Gly	Ile	Phe	Asp	Leu	Val	40
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Glu		Gln	Leu	Lys	Ala	Glu	Tyr	Pro	Val	Gly	Ala	Val	Gly	Leu	Ala	Val	55
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Ala		Gly	Phe	Leu	Asp	Pro	Glu	Cys	Glu	Val	Val	Arg	Phe	Ala	Pro	His	70
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Gly		Leu	Pro	Val	Arg	Leu	Glu	His	Asp	Ala	Asn	Ser	Ala	Ala	Trp	Gly	105
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Arg Phe Ala Pro His Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys

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											10					
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Val Thr Ala Tyr Phe Thr Arg Lys Pro Asp Val Asn Asn Pro Asp Gln												35				
											25					
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Gln Val Ala Phe Gly Thr Ser Gly His Arg Gly Phe Ala Leu Asp Ser												50				
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Tyr Arg Asn Gln Gln Pro Lys Asn Trp Val Gly Pro Leu Phe Ile Gly												85				
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cgc gat acg cac gcg ctg tcc gaa cca gcg atg atc agc gcg ctt gag											403					
Arg Asp Thr His Ala Leu Ser Glu Pro Ala Met Ile Ser Ala Leu Glu												100				
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gtc ctc att gcc aac gac gtc gaa gtg ctt gtc gac gcc gac ggc cgc											451					
Val Leu Ile Ala Asn Asp Val Glu Val Leu Val Asp Ala Asp Gly Arg												115				
											105					
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Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile Leu Arg His Asn Asp												130				
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ggc atc atc ctt ggc acc gca gga ccc tcc cgc ccc tac gcc gac ggc											547					
Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg Pro Tyr Ala Asp Gly												145				
											135					
atc gtg atc acc cca tcc cac aac cct cct cgt gat ggc gga ttc aaa											595					
Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg Asp Gly Gly Phe Lys												165				
											150					
tac aac cca gcc aac ggt ggc cct gca gat acc gac gcc acc gac tgg											643					
Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr Asp Ala Thr Asp Trp												180				
											170					
atc gcc aac cgc gcc aac gat att ctg cgc ggc gac ctt gca gac gtg											691					
Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly Asp Leu Ala Asp Val												195				
											185					
aag cga gtt cca gtt tcc ggt gtc ctc gac gag cgc acc act gcc tac											739					
Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu Arg Thr Thr Ala Tyr												210				
											200					
gac ttc aag ggc att tac atc gct gac ctg cca aac gtg gtc aac atc											787					
Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro Asn Val Val Asn Ile												225				
											215					
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Asp 230	Ala	Ile	Arg	Glu	Ala 235	Gly	Val	Arg	Ile	Gly 240	Ala	Asp	Pro	Met	Gly 245	
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aac Asn	ctc Leu	acc Thr	gtg Val	gtc Val	aac Asn	cca Pro	cac His	gtt Val	gat Asp	tcc Ser	acc Thr	ttc Phe	cgc Arg	ttc Phe	atg Met	931
aca Thr	ttg Leu	gac Asp	acc Thr	gac Asp	ggc Gly	aag Lys	atc Ile	cgc Arg	atg Met	gac Asp	tgc Cys	tcc Ser	agc Ser	cca Pro	cac His	979
gca Ala	atg Met	gca Ala	tcg Ser	ctg Leu	att Ile	gac Asp	aac Asn	cga Arg	gac Asp	aag Lys	ttc Phe	gat Asp	gtg Val	gca Ala	acc Thr	1027
ggc Gly	aac Asn	gac Asp	gcc Ala	gac Asp	gcc Ala	gac Asp	cgc Arg	cac His	ggc Gly	atc Ile	gtc Val	acc Thr	cca Pro	gac Asp	gct Ala	1075
ggc Gly	ttg Leu	atg Met	aac Asn	ccc Pro	aac Asn	cac His	tac Tyr	ctc Leu	gca Ala	gta Val	gca Ala	att Ile	gag Glu	tac Tyr	ctc Leu	1123
ttt Phe	gct Ala	cac His	cgc Arg	cca Pro	ggt Gly	tgg Trp	tcc Ser	gca Ala	gat Asp	acc Thr	gca Ala	gtg Val	ggc Gly	aaa Lys	acc Thr	1171
ctg Leu	gtc Val	agc Ser	tcc Ser	tcc Ser	atg Met	atc Ile	gac Asp	cgc Arg	gtt Val	gtg Val	gcg Ala	cag Gln	ctt Leu	ggc Gly	cgc Arg	1219
acc Thr	ctc Leu	gtt Val	gag Glu	gtt Val	cca Pro	gtc Val	gga Gly	ttc Phe	aag Lys	tgg Trp	ttt Phe	gtc Val	cca Pro	ggg Gly	ttg Leu	1267
atc Ile	tcc Ser	ggc Gly	gaa Glu	atc Ile	gga Gly	ttc Phe	ggt Gly	ggt Gly	gaa Glu	gaa Glu	tcc Ser	gca Ala	ggg Gly	gca Ala	tcc Ser	1315
ttc Phe	ctc Leu	cgc Arg	atg Met	gac Asp	ggc Gly	acc Thr	acc Thr	tgg Trp	tcc Ser	acc Thr	gac Asp	aag Lys	gac Asp	ggc Gly	ctc Leu	1363
atc Ile	ctt Leu	gac Asp	ctc Leu	ctg Leu	gca Ala	gct Ala	gag Glu	atc Ile	att Ile	gca Ala	gta Val	acc Thr	ggc Gly	aag Lys	acc Thr	1411
cca Pro	tca Ser	cag Gln	cgc Arg	tac Tyr	gca Ala	gaa Glu	ctc Leu	gcc Ala	gaa Glu	gaa Glu	ttc Phe	ggg Gly	gca Ala	cct Pro	gcc Ala	1459
tac Tyr	gcc Ala	cgc Arg	acc Thr	gat Asp	gca Ala	gaa Glu	gcc Ala	aac Asn	cga Arg	gaa Glu	caa Gln	aag Lys	gcc Ala	atc Ile	ctg Leu	1507
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 490 495 500

gga gga cta aaa gtg acc acc gaa aac gcc tgg ttc gca gca cgc cca 1651
 Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp Phe Ala Ala Arg Pro
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tcc ggc acc gaa gac aag tac aag atc tac gca gaa tcc ttc aag ggc 1699
 Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala Glu Ser Phe Lys Gly
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gaa gag cac ctc gcc cag gtt cag aag gaa gcc caa gcg ttg gtc agc 1747
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Phe Ala Leu Asp Ser Ala Phe Asn Glu Asp His Ile Leu Ala Thr Thr
 50 55 60

Gln Ala Ile Val Asp Tyr Arg Asn Gln Gln Pro Lys Asn Trp Val Gly
 65 70 75 80

Pro Leu Phe Ile Gly Arg Asp Thr His Ala Leu Ser Glu Pro Ala Met
 85 90 95

Ile Ser Ala Leu Glu Val Leu Ile Ala Asn Asp Val Glu Val Leu Val
 100 105 110

Asp Ala Asp Gly Arg Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile
 115 120 125

Leu Arg His Asn Asp Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg
 130 135 140

Pro Tyr Ala Asp Gly Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg
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Asp Gly Gly Phe Lys Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr
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[illegible]

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Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala	Phe	Pro	Asn	Pro	Glu		
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gag	cct	tct	gcg	att	gag	ttg	ttg	ttg	gaa	cgc	gca	aag	gaa	aag	aac	931	
Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	Ala	Lys	Glu	Lys	Asn		
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gct	gac	att	ttg	ttt	gcg	ctt	gat	cct	gat	gcc	gat	cgt	tgt	gct	gtg	979	
Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala	Asp	Arg	Cys	Ala	Val		
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Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	Glu	Tyr	Ser	Gly	Glu		
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gct	ttc	gct	tat	gag	gaa	gct	gtg	ggc	acc	tgc	ccg	gtt	cca	gat	gtc	1267	
Ala	Phe	Ala	Tyr	Glu	Glu	Ala	Val	Gly	Thr	Cys	Pro	Val	Pro	Asp	Val		
	375					380					385						
gtg	ccg	gat	aag	gac	ggc	atc	tct	aca	gcg	ttg	ttc	atg	gcg	tcg	tgg	1315	
Val	Pro	Asp	Lys	Asp	Gly	Ile	Ser	Thr	Ala	Leu	Phe	Met	Ala	Ser	Trp		
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gct	gcc	gaa	ctg	aag	gct	cag	ggc	gca	agc	ctg	cag	caa	aaa	ctc	aat	1363	
Ala	Ala	Glu	Leu	Lys	Ala	Gln	Gly	Ala	Ser	Leu	Gln	Gln	Lys	Leu	Asn		
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Glu	Leu	Tyr	Arg	Arg	Tyr	Gly	Tyr	Phe	Ala	Ser	Ser	Gln	Ile	Ala	Val		
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Arg	Thr	Ser	Ser	Pro	Arg	Glu	Leu	Val	Asp	His	Trp	Ile	Ala	His	Pro		
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cag	caa	gaa	ctc	att	gga	gtg	tct	gtc	acc	cca	cat	att	ctt	cct	gaa	1507	
Gln	Gln	Glu	Leu	Ile	Gly	Val	Ser	Val	Thr	Pro	His	Ile	Leu	Pro	Glu		
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Arg	Tyr	Gly	Ser	His	Thr	Phe	Ala	Ala	Thr	Thr	Ala	Glu	Val	Phe	Ala
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Gly	Ala	Gly	Phe	Glu	Val	Thr	Leu	Leu	Pro	Thr	Pro	Ser	Pro	Thr	Pro
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Ala	His	Ile	Asn	Ala	Val	Glu	Asp	Pro	Ile	Arg	Val	Pro	Arg	Val	Thr
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Val	Arg	Pro	Thr	Ala	Asp	Gln	Leu	Arg	Arg	Tyr	Val	Asp	Glu	Met	Val
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Arg	Gly	Asn	Leu	Arg	Val	Val	Tyr	Thr	Ala	Leu	His	Gly	Val	Gly	Gly

Parameter	Value	Unit
Initial Temperature	25.0	°C
Final Temperature	100.0	°C
Heating Rate	10.0	°C/min
Sample Weight	0.5000	g
Sample Name	Sample 1	
Sample ID	1	
Sample Description	Sample 1	
Sample Location	Sample 1	
Sample Date	2010-01-01	
Sample Time	10:00:00	
Sample Operator	Sample 1	
Sample Instrument	Sample 1	
Sample Method	Sample 1	
Sample Result	Sample 1	
Sample Error	Sample 1	
Sample Status	Sample 1	
Sample Comment	Sample 1	
Sample Note	Sample 1	
Sample Remark	Sample 1	
Sample Detail	Sample 1	
Sample Info	Sample 1	
Sample Data	Sample 1	
Sample Report	Sample 1	
Sample Print	Sample 1	
Sample Export	Sample 1	
Sample Import	Sample 1	
Sample Delete	Sample 1	
Sample Update	Sample 1	
Sample Insert	Sample 1	
Sample Select	Sample 1	
Sample Query	Sample 1	
Sample Table	Sample 1	
Sample View	Sample 1	
Sample Function	Sample 1	
Sample Procedure	Sample 1	
Sample Package	Sample 1	
Sample Schema	Sample 1	
Sample User	Sample 1	
Sample Role	Sample 1	
Sample Privilege	Sample 1	
Sample Permission	Sample 1	
Sample Access	Sample 1	
Sample Control	Sample 1	
Sample Security	Sample 1	
Sample Audit	Sample 1	
Sample Log	Sample 1	
Sample Trace	Sample 1	
Sample Monitor	Sample 1	
Sample Alert	Sample 1	
Sample Notification	Sample 1	
Sample Message	Sample 1	
Sample Event	Sample 1	
Sample Task	Sample 1	
Sample Job	Sample 1	
Sample Process	Sample 1	
Sample Service	Sample 1	
Sample Application	Sample 1	
Sample Component	Sample 1	
Sample Module	Sample 1	
Sample Class	Sample 1	
Sample Interface	Sample 1	
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Sample Job	Sample 1	
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Sample Component	Sample 1	
Sample Module	Sample 1	
Sample Class	Sample 1	
Sample Interface	Sample 1	

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Asp	Arg 290	Cys	Ala	Val	Gly	Ile 295	Arg	Thr	Ala	Asp	Gly 300	Gly	His	Arg	Met	
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Glu	Tyr	Ser	Gly	Glu 325	Gly	Pro	Arg	Pro	Val 330	Val	Ala	Thr	Thr	Val 335	Val	
Ser	Ser	Gln	Leu 340	Leu	Gly	Ile	Ile	Ala 345	Glu	Asp	Lys	Gly	Trp 350	Asp	Tyr	
Ser	Glu	Thr 355	Leu	Thr	Gly	Phe	Lys 360	Asn	Leu	Ser	Arg	Ala 365	Ala	Asp	Gly	
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Pro 385	Val	Pro	Asp	Val	Val 390	Pro	Asp	Lys	Asp	Gly 395	Ile	Ser	Thr	Ala	Leu 400	
Phe	Met	Ala	Ser	Trp 405	Ala	Ala	Glu	Leu	Lys 410	Ala	Gln	Gly	Ala	Ser 415	Leu	
Gln	Gln	Lys	Leu 420	Asn	Glu	Leu	Tyr	Arg 425	Arg	Tyr	Gly	Tyr	Phe 430	Ala	Ser	
Ser	Gln	Ile 435	Ala	Val	Arg	Thr	Ser 440	Ser	Pro	Arg	Glu	Leu 445	Val	Asp	His	
Trp 450	Ile	Ala	His	Pro	Gln	Gln 455	Glu	Leu	Ile	Gly	Val 460	Ser	Val	Thr	Pro	
His 465	Ile	Leu	Pro	Glu	Lys 470	Gln	Gly	Ile	Ala	Leu 475	His	Gly	Gln	Val	Gly 480	
His	Val	His	Ile	Arg 485	Ala	Ile	Gly	Arg	Val 490	Ser	Gly	Thr	Glu	Ala 495	Lys	
Ala	Lys	Leu	Tyr 500	Leu	Glu	Val	Gly	Gln 505	Ala	Ser	Ser	His	Asp 510	Glu	Ala	
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gta gga gac cgc tac gtg ctg gaa gac ctc aat gca ggt gga ttc agc 144
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 Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
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cca cag gtt ctg atc aat gtg cca gtt tcg gat aag tcc acc atc gtg 336
 Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
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 Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
 115 120 125

ggc gcc acc ggt cgc gtt ctt ctt cgt gct tct ggc acc gaa gag ctt 432
 Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
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 Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
 145 150 155 160

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Leu	Thr	Ser	Thr	Asp	Glu	Leu	Tyr	Phe	Ala	Ser	Gly	Thr	Leu	Lys	Cys
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210						215						220			
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Tyr	Leu	Glu	Lys	Leu	Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr
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Ser	Lys	Ala	Val	Pro	Glu	Val	Ile	Ala	Glu	Asn	Gly	Gly	Thr	Ala	Val
290						295						300			
Arg	Thr	Arg	Val	Gly	His	Ser	Phe	Ile	Lys	Ala	Lys	Met	Ala	Glu	Thr
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Gly	Ala	Ala	Phe	Gly	Gly	Glu	His	Ser	Ala	His	Tyr	Tyr	Phe	Thr	Glu
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Phe	Phe	Asn	Ala	Asp	Ser	Gly	Ile	Leu	Ala	Ala	Met	His	Val	Leu	Ala
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 Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
 50 55 60
 Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
 65 70 75 80
 Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
 85 90 95
 Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
 100 105 110
 Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
 115 120 125
 Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
 130 135 140
 Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
 145 150 155 160
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
 165 170 175
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
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 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
 245 250 255
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
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 Ser Lys Ala Val Pro Glu Val Ile Ala Glu
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Thr	Leu	Phe	Val	Ile	Ala	Ser	Lys	Thr	Phe	Thr	Thr	Gln	Glu	Thr	Leu						
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tcc	aac	gct	cgt	gca	gct	cgt	gct	tgg	ctg	gta	gag	aag	ctc	ggt	gaa						787
Ser	Asn	Ala	Arg	Ala	Ala	Arg	Ala	Trp	Leu	Val	Glu	Lys	Leu	Gly	Glu						
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gag	gct	gtc	gcg	aag	cac	ttc	gtc	gca	gtg	tcc	acc	aat	gct	gaa	aag						835
Glu	Ala	Val	Ala	Lys	His	Phe	Val	Ala	Val	Ser	Thr	Asn	Ala	Glu	Lys						
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gtc	gca	gag	ttc	ggt	atc	gac	acg	gac	aac	atg	ttc	ggc	ttc	tgg	gac						883
Val	Ala	Glu	Phe	Gly	Ile	Asp	Thr	Asp	Asn	Met	Phe	Gly	Phe	Trp	Asp						
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tgg	gtc	gga	ggt	cgt	tac	tcc	gtg	gac	tcc	gca	gtt	ggt	ctt	tcc	ctc						931
Trp	Val	Gly	Gly	Arg	Tyr	Ser	Val	Asp	Ser	Ala	Val	Gly	Leu	Ser	Leu						
			265					270					275								
atg	gca	gtg	atc	ggc	cct	cgc	gac	ttc	atg	cgt	ttc	ctc	ggt	gga	ttc						979
Met	Ala	Val	Ile	Gly	Pro	Arg	Asp	Phe	Met	Arg	Phe	Leu	Gly	Gly	Phe						
		280					285					290									
cac	gcg	atg	gat	gaa	cac	ttc	cgc	acc	acc	aag	ttc	gaa	gag	aac	gtt						1027
His	Ala	Met	Asp	Glu	His	Phe	Arg	Thr	Thr	Lys	Phe	Glu	Glu	Asn	Val						
	295					300					305										
cca	atc	ttg	atg	gct	ctg	ctc	ggt	gtc	tgg	tac	tcc	gat	ttc	tat	ggt						1075
Pro	Ile	Leu	Met	Ala	Leu	Leu	Gly	Val	Trp	Tyr	Ser	Asp	Phe	Tyr	Gly						
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Ala	Glu	Thr	His	Ala	Val	Leu	Pro	Tyr	Ser	Glu	Asp	Leu	Ser	Arg	Phe						
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gct	gct	tac	ctc	cag	cag	ctg	acc	atg	gaa	tca	aat	ggc	aag	tca	gtc						1171
Ala	Ala	Tyr	Leu	Gln	Gln	Leu	Thr	Met	Glu	Ser	Asn	Gly	Lys	Ser	Val						
			345					350					355								
cac	cgc	gac	ggc	tcc	cct	gtt	tcc	act	ggc	act	ggc	gaa	att	tac	tgg						1219
His	Arg	Asp	Gly	Ser	Pro	Val	Ser	Thr	Gly	Thr	Gly	Glu	Ile	Tyr	Trp						
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ggt	gag	cct	ggc	aca	aat	ggc	cag	cac	gct	ttc	ttc	cag	ctg	atc	cac						1267
Gly	Glu	Pro	Gly	Thr	Asn	Gly	Gln	His	Ala	Phe	Phe	Gln	Leu	Ile	His						
	375					380					385										
cag	ggc	act	cgc	ctt	gtt	cca	gct	gat	ttc	att	ggt	ttc	gct	cgt	cca						1315
Gln	Gly	Thr	Arg	Leu	Val	Pro	Ala	Asp	Phe	Ile	Gly	Phe	Ala	Arg	Pro						
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aag	cag	gat	ctt	cct	gcc	ggt	gag	cgc	acc	atg	cat	gac	ctt	ttg	atg						1363
Lys	Gln	Asp	Leu	Pro	Ala	Gly	Glu	Arg	Thr	Met	His	Asp	Leu	Leu	Met						
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agc	aac	ttc	ttc	gca	cag	acc	aag	gtt	ttg	gct	ttc	ggt	aag	aac	gct						1411
Ser	Asn	Phe	Phe	Ala	Gln	Thr	Lys	Val	Leu	Ala	Phe	Gly	Lys	Asn	Ala						
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 gtc atg cca ggt aat cgc cca acc acc acc att ttg gcg gag gaa ctt 1507
 Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu Glu Leu
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 acc cct tct att ctg ggt gcg ttg atc gct ttg tac gaa cac atc gtg 1555
 Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Ile Val
 470 475 480 485
 atg gtt cag ggc gtg att tgg gac atc aac tcc ttc gac caa tgg ggt 1603
 Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly
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 gtt gaa ctg ggc aaa cag cag gca aat gac ctg gct ccg gct gtc tct 1651
 Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala Val Ser
 505 510 515
 ggt gaa gag gat gtt gac tcg gga gat tct tcc act gat tca ctg att 1699
 Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile
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<213> Corynebacterium glutamicum

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 35 40 45
 Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
 50 55 60
 Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
 65 70 75 80
 Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
 85 90 95
 Leu Arg Leu Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
 100 105 110
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 115 120 125
 Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys

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Val Lys Leu Val Ile																5
gag gcc gac ggc ggc tcc cgc gga aac ccc ggc gtc gcc ggc tcc ggc																163
Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly Val Ala Gly Ser Gly																20
acc gtg gtg tac tcc gac aac aaa gca gaa gtt ctc aaa gaa atc gcc																211
Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val Leu Lys Glu Ile Ala																35
tat gtt gtc gga aca aaa gcc acc aac aac gtc gcc gaa tac cgc gga																259
Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val Ala Glu Tyr Arg Gly																40
cta ctc gaa ggc ctc aaa gca gcc cgc gag ctc ggc gct acc tcc gtg																307
Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu Gly Ala Thr Ser Val																55
gat gtc tac atg gac tcc aaa ctt gtc gtt gaa caa atg tcc ggc cgg																355
Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu Gln Met Ser Gly Arg																70
tgg aaa atc aaa cac ccc gac atg aaa gtt cta gcg atc gaa gcc aag																403
Trp Lys Ile Lys His Pro Asp Met Lys Val Leu Ala Ile Glu Ala Lys																90
gag att gct tcc gaa atc ggg tcc gtt tct tat acg tgg att ccg cgt																451
Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr Thr Trp Ile Pro Arg																105
gag aaa aac aaa cga gct gac gca ttg tcc aac gtg gcg atg gat gct																499
Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn Val Ala Met Asp Ala																120

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Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys Glu Asp Leu Asn Cys	
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Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala Thr Thr Asp Pro Thr	
170 175 180	
cgt ttc ttg ttg ctt cgc cac ggc caa act gct atg tca gtg gca cgc	691
Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala Met Ser Val Ala Arg	
185 190 195	
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Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser Glu Leu Gly Glu Lys	
200 205 210	
caa gca gca gcg gca gca cga cga ctc gct caa acc ggt ggc atc gac	787
Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln Thr Gly Gly Ile Asp	
215 220 225	
gct att gtg agt tct ccg ctc acc cgc acg atg caa acc gca gaa gca	835
Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met Gln Thr Ala Glu Ala	
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Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val Ile Asp Asp Leu Ile	
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gaa act gac ttt gga ctg tgg gat gga aaa tca ttt tca gaa gcc cac	931
Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser Phe Ser Glu Ala His	
265 270 275	
gaa caa gat cca gaa ctg cac acc aag tgg ctc act gac tca tct gta	979
Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu Thr Asp Ser Ser Val	
280 285 290	
gcc cca ccc ggt ggt gag tcc ctg cag acg gtt aat cga cgt gtg aaa	1027
Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val Asn Arg Arg Val Lys	
295 300 305	
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Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly Ala Ala Asn Val Leu	
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gtg gtc agc cac gtc acc cca atc aaa gcc atc atg agg caa gca ttg	1123
Val Val Ser His Val Thr Pro Ile Lys Ala Ile Met Arg Gln Ala Leu	
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Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His Leu Asp Leu Ala Ser	
345 350 355	
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Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro Thr Cys Val Arg Leu	
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Met Glu Asp Met Arg
1 5

att gct act ctc acg tca ggc ggc gac tgc ccc gga cta aac gcc gtc 163
Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val
10 15 20

atc cga gga atc gtc cgc aca gcc agc aat gaa ttt ggc tcc acc gtc 211
Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val
25 30 35

Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg
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 Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys
 295 300 305

gtt gtt gct ttg aag ggt gag agc att gag atg atc acc ttt gaa gaa 1075
 Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu
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gca gtc gga acc ttg aag gaa gtt cca ttc gaa cgc tgg gtt act gcc 1123
 Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val Thr Ala
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 35 40 45

Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
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Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
 65 70 75 80

Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala
 85 90 95

Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
 100 105 110

Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
 115 120 125

Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
 130 135 140

Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr
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Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
 165 170 175

Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
 180 185 190

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 260 265 270
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 Met Ile Ile Thr Phe
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 Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser Leu Gly Glu Glu Leu
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 Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val Thr Ala Val Ala Gly
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 Gly Lys Gly Ile Asn Val Ala His Ala Val Leu Leu Ala Gly Phe Glu
 40 45 50
 acc ttg gct gtg ttc cca gcc ggc aag ctc gac ccc ttc gtc cca ctg 307
 Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp Pro Phe Val Pro Leu
 55 60 65
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 Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val Val Ile Asn Lys Asn
 70 75 80 85
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 Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp Gly Thr Thr Thr Lys
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<212> PRT

<213> *Corynebacterium glutamicum*

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Thr Ala Val Ala Gly Gly Lys Gly Ile Asn Val Ala His Ala Val Leu
          35           40           45

Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp
          50           55           60

Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val
          65           70           75           80

Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp
          85           90           95

Gly Thr Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln
          100          105          110

Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu
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Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val
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Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp
          145          150          155          160

Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly
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Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn
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Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu
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Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp
          210          215          220

Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala
          225          230          235          240

Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser
          245          250          255

Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu
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Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly
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gtt gct tcc gca gct gac gct cag gaa gtg tgc aag gct atc cgc ggt 691
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 185 190 195

ctg atc gtg gag ctt gca ggc gac gag gtc gct gag ggc ctg cgt att 739
 Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala Glu Gly Leu Arg Ile
 200 205 210

ctt tac ggt ggt tct gtt aag gca gaa acc gtc gct gag atc gtc ggt 787
 Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val Ala Glu Ile Val Gly
 215 220 225

cag cct gac gtc gac ggc gga ctt gtc ggt ggc gct tcc ctc gac ggt 835
 Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly Ala Ser Leu Asp Gly
 230 235 240 245

gaa gca ttc gcc aag ctg gct gcc aac gct gcg agc gtt gct 877
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Lys Glu Tyr Phe Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
 35 40 45

Asp Ile Arg Ser Val Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val
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Thr Phe Gly Ala Gln Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr
 65 70 75 80

Gly Glu Val Ser Ala Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val
 85 90 95

Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
 100 105 110

Leu Val Ala Ala Lys Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro
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Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
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Met Thr His Asn His																1 5
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Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu																
10 15 20																
atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt								211								
Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly																
25 30 35																
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Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg																
40 45 50																
tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg								307								
Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu																
55 60 65																
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70 75 80 85																

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 Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
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 Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
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 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
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 Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
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 Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
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Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly
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 Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
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 Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
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 Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
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 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
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 Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
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 Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
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 Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
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 Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
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 His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
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 Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
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 Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
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Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
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 Met Thr Ile Arg Val
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 Asp Asn Lys Thr Leu Ser Thr Leu Lys Phe Asp Ser Ile Met Gly
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 Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp Ser Ile Thr Val Gly
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 Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp Pro Lys Asn Leu Asp
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 Trp Ala Ala His Asn Val Asp Ile Val Ile Glu Ser Thr Gly Phe Phe
 90 95 100

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<212> PRT

<213> *Corynebacterium glutamicum*

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Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
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Ser Thr Gly Phe Phe Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu
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Ala Thr Phe Val Tyr Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn
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His Asn Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
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His Arg Asp Leu Arg Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro
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Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly
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Asp Ser His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly
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Val	Glu	Thr	Glu 185	Ile	Ser	Val	Leu	Glu	Lys 190	Ile	Ala	Glu	Ser	Pro	Glu	
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Gln	Ser	Leu	Leu	Gln 250	Glu	Glu	Met	Lys	Ala 255	Thr	Cys	Thr	Asp	Leu 260	Leu	
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Glu	Tyr	Leu	Glu	Gly	Lys	Glu	Leu	Pro	Gly	Val	Ala	Ile	Leu	Ala	Gln	

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Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu Asp Gly Thr Ala Asn	
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Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly Val Ser Met Ala Val	
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Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro Leu Phe Arg Tyr Ile	
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Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile Lys Glu Lys Gly Leu	
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Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp Asp Trp Glu Gly Tyr	
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Met	Leu	Ser	Gly	Glu	Thr	Ser	Val	Gly	Lys	Asp	Pro	His	Asn	Val	Val		
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Arg	Thr	Met	Ser	Arg	Ile	Val	Arg	Phe	Ala	Glu	Thr	Asp	Gly	Arg	Val		
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ttc	acc	acc	tct	ggt	gat	acc	gca	aag	cgt	gtg	gct	cgt	ctg	cac	agc	1267	
Phe	Thr	Thr	Ser	Gly	Asp	Thr	Ala	Lys	Arg	Val	Ala	Arg	Leu	His	Ser		
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His	Leu	Pro	Leu	Leu	Val	Phe	Thr	Pro	Asn	Glu	Ala	Val	Arg	Ser	Glu		
390					395					400					405		
ctg	gcg	ctg	acc	tgg	ggt	gca	acc	acc	ttc	ctg	tgt	cca	cct	gtc	agc	1363	
Leu	Ala	Leu	Thr	Trp	Gly	Ala	Thr	Thr	Phe	Leu	Cys	Pro	Pro	Val	Ser		
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gat	acc	gat	gac	atg	atg	cgc	gaa	gtc	gac	cgt	gct	ctt	tta	gca	atg	1411	
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cca gaa tgg ttc gac aaa cta gaa atc ggc agc gtc atc aac gtc cca Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser Val Ile Asn Val Pro 265 270 275			931
gac acc cgc gga tcc cgc cga gca ttc acc gtg acc agg gtt ttt gat Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp 280 285 290			979
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aac ctc cca gac tcc gaa ctt cca ctc cca agc ctc act gaa gaa gac Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser Leu Thr Glu Glu Asp 425 430 435			1411
ctc caa cac ctg cgc ttt gtc gtc aaa tac gcc gac atc gca gcc atc Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala Asp Ile Ala Ala Ile 440 445 450			1459
tcc ttc atc cga aac gtc gcc gac gtg gaa tac ctc ctc caa gca ctc Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu 455 460 465			1507

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 aaa atc gag acc atc cca ggc tac gaa ggc ctc gcc caa atc ctc ctg 1603
 Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu Ala Gln Ile Leu Leu
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 Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala Arg Gly Asp
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 Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val Met Leu Asn
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 aag gga cca cac atc aac gac gcc atc aag gtc ctc acc gaa atg agc 1891
 Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr Glu Met Ser
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 cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg ctg cgc aag 1939
 Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu Leu Arg Lys
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 Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
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 Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
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 Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala

002290-0720950

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Asn	Leu	Ala	Arg	Ile	Asn	Cys	Ala	His	Asp	Asp	Glu	Thr	Val	Trp	Lys
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Gln	Met	Ile	Asp	Asn	Val	His	Thr	Val	Ala	Glu	Glu	Val	Gly	Arg	Glu
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 Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
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 Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg
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 Ala Gln Ile Leu Leu Thr Gly Met Arg His Glu Asn Phe Gly Ile Met
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 Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala
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 530 535 540
 Thr Ile Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu
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 Pro Ser Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu
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 Cys Val Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val
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 Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val

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Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser				
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Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val				
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Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr				
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gaa atg agc cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg				336
Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu				
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Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val				
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Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr				
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Pro	Ile	Glu	Val	Thr	Pro	Glu	Trp	Phe	Asp	Lys	Leu	Glu	Ile	Gly	Ser
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Thr	Arg	Val	Phe	Asp	Gly	Ala	Val	Leu	Ala	Glu	Gly	Pro	Gln	Lys	Ala
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Val	Glu	Leu	Glu	Val	Thr	His	Ala	Arg	Pro	Gln	Gly	Val	Asn	Leu	Ala
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Ala	Tyr	Lys	Gly	Ile	Asn	Leu	Pro	Asp	Ser	Glu	Leu	Pro	Leu	Pro	Ser
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Leu	Thr	Glu	Glu	Asp	Leu	Gln	His	Leu	Arg	Phe	Val	Val	Lys	Tyr	Ala
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 Met Phe Gln Glu Arg Ile Thr His Tyr Phe Gln Asn Trp Glu Pro Met
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 Ser Leu Glu Phe Lys Pro Leu Pro Asp Tyr Val Pro Ile Asp Asp Ile
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 Val Ser Gly Lys Ala Lys Asp Gly Thr Glu Val Leu Met Glu Asn Phe
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 Phe Leu Asn Leu Gly Tyr Ile Ala Tyr Leu Asp Phe Phe Asn Phe Cys
 195 200 205
 Lys Glu Val Phe Pro Asp Ile Pro Asp Gln Ser Ile Ser Met Met Val
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 Gln Gly Val Asp Met Glu Leu Phe Arg Pro Asp Asp Glu Leu Lys Ile
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 Pro Asp Asp Pro Gln Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly
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 Gly Ala Thr Trp Ile Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe
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 Asn Phe Thr Val Gly Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile
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 Glu Lys Glu Arg Val Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu
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 Gln Leu Ala Gln Phe Asp Ala Lys Cys Gly Leu Ala Ala Thr Ala Tyr
 355 360 365
 Pro Tyr Val Glu Asn His Asn Phe Tyr Ile Glu His Trp Thr Met Ser

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 Val Arg Asp Val Leu Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala
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 Arg Lys Ala Ile Val Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala
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Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met Glu Arg Cys Gly Gly
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Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr Ala Glu Asp Leu Pro
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Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn Gly Asp Arg Ser Lys
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Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile
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Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg
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Gln Ser Asp Ile Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala
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Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys
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gct gct tct tgt ggt cct gga aac aca cac ctg att cag ggt ctt tat 355
Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr
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gat tcg cat cga aat ggt gcg aag gtg ttg gcc atc gct agc cat att 403
Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile
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Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu
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Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly
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Glu Gln Gly Glu Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala
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Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp	
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Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro	
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Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn	
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Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly	
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Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys	
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Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val	
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Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His	
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Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala	
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Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
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Val	Glu	Lys	His	Val	Pro	Ile	His	Pro	Glu	Tyr	Val	Ala	Ser	Ile	Leu
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Asn	Glu	Leu	Ala	Asp	Lys	Asp	Ala	Val	Phe	Thr	Val	Asp	Thr	Gly	Met
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Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val	
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His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val	
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Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu	
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Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu	
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Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly	
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 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
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act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt 144
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
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ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
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cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80

cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95

ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336
 Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
 100 105 110

aac acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggc gca ggc 384
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
 115 120 125

tgg tct gtg atc aag gtt gtt tgg ggt cgc gag tgg gat gaa ctt ctg 432
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140

gag aag gac cag gat ggt gca ctt gtt gag atc atg aac aac acc tcc 480
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
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 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
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Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn	
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Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr	
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cgc aag gtt tac gca gcc tac aag cga gct ctt gag acc aag gat cgc	672
Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg	
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cca acc gtc atc ctt gct cac acc att aag ggc tac gga ctc ggc cac	720
Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His	
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Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu	
245 250 255	
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Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp	
260 265 270	
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Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly	
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Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu	
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Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val	
305 310 315 320	
cca cca ctg gat aag ctt cgc tct gtc cgt aag ggc tcc ggc aag cag	1008
Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln	
325 330 335	
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Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met	
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Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu	
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Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr	
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Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu	
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tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac	1248
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn	
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1287

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 35 40 45
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95
 Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
 100 105 110
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
 115 120 125
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190
 Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
 195 200 205
 Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
 210 215 220
 Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
 225 230 235 240
 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
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 Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
 260 265 270

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Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
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 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
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 Met Ala Lys Arg Ile Val Ile Ile Gly
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 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
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 gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 210
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
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 acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 258
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
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Lys Val Asp Arg Ser Pro Ala Pro Thr Ser Pro Val Cys Thr Gln Gln
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 gtg act gta ctg acc tat tcc cac tgg cgt ccg ttg cag cga tgc agg 1074
 Val Thr Val Leu Thr Tyr Ser His Trp Arg Pro Leu Gln Arg Cys Arg
 315 320 325
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 35 40 45
 Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
 50 55 60
 Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65 70 75 80
 Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
 85 90 95
 Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly
 100 105 110
 Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile
 115 120 125
 Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu
 130 135 140
 Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu
 145 150 155 160
 Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu
 165 170 175
 Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala
 180 185 190
 Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val
 195 200 205
 Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp
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Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His
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Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val
245 250 255

Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr
260 265 270

Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly
275 280 285

Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Ser Pro Ala
290 295 300

Pro Thr Ser Pro Val Cys Thr Gln Gln Val Thr Val Leu Thr Tyr Ser
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His Ser Val Lys Ala
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Met Ala Lys Arg Ile Val Ile Ile Gly

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Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly

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Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val

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35

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acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 259

Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile

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aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 307

Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu

60

65

70

gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac 355

Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp

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ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu 190 195 200			691
ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His 205 210 215			739
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 Arg Leu Lys Thr Val Ala Thr Ala Val Phe Thr Arg Pro Glu Ile Ala
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 Ala Val Gly Ile Thr His Ala Gln Val Asp Ser Gly Glu Val Ser Ala
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 Arg Val Ile Val Leu Pro Leu Ala Thr Asn Pro Arg Ala Lys Met Arg
 380 385 390
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 Ser Leu Arg His Gly Phe Val Lys Leu Phe Cys Arg Arg Asn Ser Gly
 395 400 405
 ctg atc atc ggt ggt gtc gtg gtg gca ccg acc gcg tct gag ctg atc 1363
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 410 415 420 425
 cta ccg atc gct gtg gca gtg acc aac cgt ctg aca gtt gct gat ctg 1411
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 35 40 45
 Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
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 Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65 70 75 80

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Gln	Thr	Ala	Leu	Ile	Arg	Val	Ala	Arg	Pro	Arg	Ile	Glu	Asp	Glu	Ile		
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Thr	His	Arg	Ala	Ala	Glu	Thr	Val	Leu	Lys	Tyr	Tyr	Ala	Arg	Gln	Leu		
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cat	tcc	ctc	gag	cat	gag	ctc	agc	ctg	tcg	gac	cgc	atg	aat	aag	gtc	1027	
His	Ser	Leu	Glu	His	Glu	Leu	Ser	Leu	Ser	Asp	Arg	Met	Asn	Lys	Val		
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acc	ccg	cag	ctg	ctt	gcg	ctg	gca	gat	gca	ggg	cac	aac	gac	gtg	cca	1075	
Thr	Pro	Gln	Leu	Leu	Ala	Leu	Ala	Asp	Ala	Gly	His	Asn	Asp	Val	Pro		
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agc	cgc	gtg	gat	gag	cct	tat	cga	cgc	gcc	gtc	cat	ggc	gtt	cgc	gga	1123	
Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Val	His	Gly	Val	Arg	Gly		
				330					335					340			
cgt	atc	ctc	gcg	acg	acg	gcc	gag	ctg	atc	ggc	gag	gac	gcc	gtt	gag	1171	
Arg	Ile	Leu	Ala	Thr	Thr	Ala	Glu	Leu	Ile	Gly	Glu	Asp	Ala	Val	Glu		
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ggc	gtg	tgg	ttc	aag	gtc	ttt	act	cca	tac	gca	tct	ccg	gaa	gaa	ttc	1219	
Gly	Val	Trp	Phe	Lys	Val	Phe	Thr	Pro	Tyr	Ala	Ser	Pro	Glu	Glu	Phe		

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tcc tac gac gcg att ctt gcc cag ccc agg ggg gct gtc caa ggt tcc	2035
Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly Ala Val Gln Gly Ser	
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gtg cgc atc acc gag cag ggc gag atc atc tcc gct aag tac ggc aac	2083
Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn	
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ccc gaa acc gcg cgc cga aac ctc gaa gcc ctg gtc tca gcc acg ctt	2131
Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu	
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Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr Asp His Gln Arg Ala	
680 685 690	
tac gac atc atg agt gag atc tct gag ctc agc ttg aag aag tac gcc	2227
Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser Leu Lys Lys Tyr Ala	
695 700 705	
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Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp Tyr Phe Thr Gln Ser	
710 715 720 725	
acg ccg ctg cag gag att gga tcc ctc aac atc gga tcc agg cct tcc	2323
Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser	
730 735 740	
tca cgc aag cag acc tcc tcg gtg gaa gat ttg cga gcc atc cca tgg	2371
Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu Arg Ala Ile Pro Trp	
745 750 755	
gtg ctc agc tgg tca cag tct cgt gtc atg ctg cca ggc tgg ttt ggt	2419
Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly	
760 765 770	
gtc gga acc gca tta gag cag tgg att ggc gaa ggg gag cag gcc acc	2467
Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu Gly Glu Gln Ala Thr	
775 780 785	
caa cgc att gcc gag ctg caa aca ctc aat gag tcc tgg cca ttt ttc	2515
Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu Ser Trp Pro Phe Phe	
790 795 800 805	
acc tca gtg ttg gat aac atg gct cag gtg atg tcc aag gca gag ctg	2563
Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu	
810 815 820	
cgt ttg gca aag ctc tac gca gac ctg atc cca gat acg gaa gta gcc	2611
Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro Asp Thr Glu Val Ala	
825 830 835	
gag cga gtc tat tcc gtc atc cgc gag gag tac ttc ctg acc aag aag	2659
Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr Phe Leu Thr Lys Lys	
840 845 850	

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Leu	Glu	Glu	Ile	Pro	Arg	Ile	Asn	Arg	Asp	Val	Ala	Val	Glu	Leu	Arg
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Glu	Arg	Phe	Gly	Glu	Gly	Val	Pro	Leu	Lys	Pro	Val	Val	Lys	Pro	Gly
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Thr	Val	Glu	Tyr	Ser	Thr	His	Arg	Ala	Ala	Glu	Thr	Val	Leu	Lys	Tyr
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Tyr	Ala	Arg	Gln	Leu	His	Ser	Leu	Glu	His	Glu	Leu	Ser	Leu	Ser	Asp
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Arg	Met	Asn	Lys	Val	Thr	Pro	Gln	Leu	Leu	Ala	Leu	Ala	Asp	Ala	Gly
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His	Asn	Asp	Val	Pro	Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Val
			325						330					335	
His	Gly	Val	Arg	Gly	Arg	Ile	Leu	Ala	Thr	Thr	Ala	Glu	Leu	Ile	Gly
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Glu	Asp	Ala	Val	Glu	Gly	Val	Trp	Phe	Lys	Val	Phe	Thr	Pro	Tyr	Ala
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Ser	Pro	Glu	Glu	Phe	Leu	Asn	Asp	Ala	Leu	Thr	Ile	Asp	His	Ser	Leu
	370					375					380				
Arg	Glu	Ser	Lys	Asp	Val	Leu	Ile	Ala	Asp	Asp	Arg	Leu	Ser	Val	Leu
385					390					395					400
Ile	Ser	Ala	Ile	Glu	Ser	Phe	Gly	Phe	Asn	Leu	Tyr	Ala	Leu	Asp	Leu
			405						410					415	
Arg	Gln	Asn	Ser	Glu	Ser	Tyr	Glu	Asp	Val	Leu	Thr	Glu	Leu	Phe	Glu
			420					425					430		
Arg	Ala	Gln	Val	Thr	Ala	Asn	Tyr	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Lys
		435					440					445			
Leu	Glu	Val	Leu	Leu	Lys	Glu	Leu	Arg	Ser	Pro	Arg	Pro	Leu	Ile	Pro
	450					455					460				
His	Gly	Ser	Asp	Glu	Tyr	Ser	Glu	Val	Thr	Asp	Arg	Glu	Leu	Gly	Ile
465					470					475					480
Phe	Arg	Thr	Ala	Ser	Glu	Ala	Val	Lys	Lys	Phe	Gly	Pro	Arg	Met	Val
			485						490					495	
Pro	His	Cys	Ile	Ile	Ser	Met	Ala	Ser	Ser	Val	Thr	Asp	Val	Leu	Glu
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 Asn Pro Arg Gly Thr Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu
 530 535 540
 Asp Leu Gln Ala Gly Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp
 545 550 555 560
 Leu Tyr Arg Asn Tyr Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met
 565 570 575
 Leu Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn
 580 585 590
 Trp Ala Leu Tyr Asp Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser
 595 600 605
 Ala Gly Val Lys Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly
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 Arg Gly Gly Gly Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly
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 Ala Val Gln Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser
 645 650 655
 Ala Lys Tyr Gly Asn Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu
 660 665 670
 Val Ser Ala Thr Leu Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr
 675 680 685
 Asp His Gln Arg Ala Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser
 690 695 700
 Leu Lys Lys Tyr Ala Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp
 705 710 715 720
 Tyr Phe Thr Gln Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile
 725 730 735
 Gly Ser Arg Pro Ser Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu
 740 745 750
 Arg Ala Ile Pro Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu
 755 760 765
 Pro Gly Trp Phe Gly Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu
 770 775 780
 Gly Glu Gln Ala Thr Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu
 785 790 795 800
 Ser Trp Pro Phe Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met
 805 810 815
 Ser Lys Ala Glu Leu Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro
 820 825 830

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Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
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 Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
 65 70 75 80
 Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
 85 90 95
 Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
 100 105 110
 Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
 115 120 125
 Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
 130 135 140
 Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
 145 150 155 160
 Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
 165 170 175
 Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
 180 185 190
 Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
 195 200 205
 Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
 210 215 220
 Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
 225 230 235 240
 Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
 245 250 255
 Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(916)

<223> FRXA02326

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 Met Leu Gly Arg Pro

003290"0420960

[illegible]

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Ala Thr Ile Thr	Ala Ser Val Asp Gly Lys Ile Asp Arg Val	Val Val Val				
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Pro Ala Ala Thr	Lys Val Glu Gly Gly Asp Leu Ile Val	Val Val Ser				
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 Leu Leu Ala Thr Arg
 1 5
 gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg 163
 Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
 10 15 20
 act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat 211
 Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
 25 30 35
 gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag 259
 Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
 40 45 50
 ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc 307
 Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
 55 60 65
 cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg 355
 Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
 70 75 80 85
 ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc 403
 Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
 90 95 100
 gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc 451
 Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
 105 110 115
 ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt 499
 Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
 120 125 130

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gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta 547
Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
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aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att 595
Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
150 155 160 165

aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc 643
Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
170 175 180

acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac 691
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
185 190 195

gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct 739
Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala
200 205 210

ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac 787
Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His
215 220 225

ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc 835
Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
230 235 240 245

cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg 883
Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
250 255 260

tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc 931
Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
265 270 275

cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag 979
Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
280 285 290

ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt 1027
Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg
295 300 305

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caa 1083

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<212> PRT
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 Leu Leu Ala Thr Arg
 1 5
 gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg 163
 Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
 10 15 20
 act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat 211
 Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
 25 30 35
 gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag 259
 Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
 40 45 50
 ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc 307
 Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
 55 60 65
 cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg 355
 Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
 70 75 80 85
 ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc 403
 Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
 90 95 100
 gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc 451
 Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
 105 110 115
 ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt 499
 Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
 120 125 130
 gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta 547
 Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
 135 140 145
 aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att 595
 Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
 150 155 160 165
 aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc 643
 Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
 170 175 180
 acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac 691

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Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
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Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
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Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
    130                      135                      140

Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
    145                      150                      155                      160

His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
    165                      170                      175

Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
    180                      185                      190

His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
    195                      200                      205

Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
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Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
    225                      230                      235                      240

Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
    245                      250                      255

Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
    260                      265                      270

Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
    275                      280                      285

Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu
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Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg							
		250		255		260	
cac caa aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa							931
His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu							
		265		270		275	
ctg cgt gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att							979
Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile							
		280		285		290	
ggt tac cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc							1027
Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly							
		295		300		305	
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Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr							
		310		315		320	325
gtg act gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc							1123
Val Thr Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg							
		330		335		340	
ttg gct gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag							1171
Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys							
		345		350		355	
atc aag acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat							1219
Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp							
		360		365		370	
cca aac aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc							1267
Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg							
		375		380		385	
tca cca ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt							1315
Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly							
		390		395		400	405
ggc gaa atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc							1363
Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys							
		410		415		420	
cgt ggt tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg							1411
Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu							
		425		430		435	
gct gag ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt							1459
Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg							
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Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly							
		455		460		465	
ttc att gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat							1555
Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp							
		470		475		480	485

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Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val
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 Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile
 225 230 235 240
 Leu Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys
 245 250 255
 Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln
 260 265 270
 His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys
 275 280 285
 Phe Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu
 290 295 300
 Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile
 305 310 315 320
 Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val
 325 330 335
 Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly
 340 345 350
 Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg
 355 360 365
 Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr
 370 375 380
 Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly
 385 390 395 400
 Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu
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 Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg
 420 425 430
 Ala Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn
 435 440 445
 Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys
 450 455 460
 Arg Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala
 465 470 475 480
 Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp
 485 490 495
 Val Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala
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 Pro Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly
 515 520 525
 Ser Arg Asp Arg

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530

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 <223> FRXA02328

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 Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala
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gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc cag ctt 144
 Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
 35 40 45

gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca acc cca 192
 Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro
 50 55 60

gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc gcc gcg 240
 Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala
 65 70 75 80

aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc aaa aac 288
 Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn
 85 90 95

atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc atc ttt 336
 Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe
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gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt gtt gct 384
 Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala
 115 120 125

tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt gaa gct 432
 Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala
 130 135 140

gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct gtg att 480
 Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile
 145 150 155 160

aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act gga gaa 528
 Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu
 165 170 175

gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt cac caa 576
 Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln
 180 185 190

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cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac	163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His	
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Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
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aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
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Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
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ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
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gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
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Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
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gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
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gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
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tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
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gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc	883

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Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
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 gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931
 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275
 ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290
 acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
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 gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg 1075
 Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala
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 Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile
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 acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag 1171
 Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln
 345 350 355
 ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc 1219
 Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro
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 gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
 375 380 385
 aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
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<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

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 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

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Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser
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Leu Pro Val Glu Ala Pro Ile Phe
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<212> DNA

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<222> (1)..(288)

<223> FRXA01048

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1 5 10 15

att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96
Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
20 25 30

atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144
Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
35 40 45

tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192
Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
50 55 60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240
Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
65 70 75 80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288
Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
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35 40 45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro

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Met Thr Ile Asp Leu 1 5															
cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163															
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His 10 15 20															
gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211															
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met 25 30 35															
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259															
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu 40 45 50															
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307															
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly 55 60 65															
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Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly 70 75 80 85															
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403															
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln 90 95 100															
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Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp 105 110 115															
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct 499															
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro 120 125 130															

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 Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
 135 140 145

 gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595
 Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
 150 155 160 165

 gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643
 Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
 170 175 180

 tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att 691
 Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
 185 190 195

 tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac 739
 Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
 200 205 210

 gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac 787
 Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
 215 220 225

 gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag 835
 Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
 230 235 240 245

 acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883
 Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
 250 255 260

 gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931
 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

 ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

 acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

 gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063
 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
 310 315 320

<210> 128

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

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Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
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<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1042)

<223> RXA02694

<400> 129

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                                         Met Lys Glu Thr Val
                                         1      5

ggt aac aag att gtc ctc att ggc gca gga gat gtt gga gtt gca tac 163
Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp Val Gly Val Ala Tyr
                        10                        15                        20

gca tac gca ctg atc aac cag ggc atg gca gat cac ctt gcg atc atc 211
Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp His Leu Ala Ile Ile
                        25                        30                        35

gac atc gat gaa aag aaa ctc gaa ggc aac gtc atg gac tta aac cat 259
Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val Met Asp Leu Asn His
                        40                        45                        50

ggt gtt gtg tgg gcc gat tcc cgc acc cgc gtc acc aag ggc acc tac 307
Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val Thr Lys Gly Thr Tyr
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gct gac tgc gaa gac gca gcc atg gtt gtc att tgt gcc ggc gca gcc 355
Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile Cys Ala Gly Ala Ala
                        70                        75                        80                        85

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Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val Asp Lys Asn Val Lys
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Ile Met Lys Ser Ile Val Gly Asp Val Met Asp Ser Gly Phe Asp Gly
                        105                        110                        115

atc ttc ctc gtg gcg tcc aac cca gtg gat atc ctg acc tac gca gtg 499
Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile Leu Thr Tyr Ala Val
                        120                        125                        130

tgg aaa ttc tcc ggc ttg gaa tgg aac cgc gtg atc ggc tcc gga act 547
Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val Ile Gly Ser Gly Thr
                        135                        140                        145

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Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu Gly Glu Leu Tyr Glu
                        150                        155                        160                        165

gtg gca cca agc tcc gtc cac gcc tac atc atc ggc gaa cac ggc gac 643
Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile Gly Glu His Gly Asp
                        170                        175                        180

act gaa ctt cca gtc ctg tcc tcc gcg acc atc gca ggc gta tcg ctt 691
Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile Ala Gly Val Ser Leu
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 att ttc gaa gac acc cgc gac gct gcc tat cac att atc gac gcc aag 787
 Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His Ile Ile Asp Ala Lys
 215 220 225
 ggc tcc act tcc tac ggc atc ggc atg ggt ctt gct cgc atc acc cgc 835
 Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu Ala Arg Ile Thr Arg
 230 235 240 245
 gca atc cta cag aac caa gac gtt gca gtc cca gtc tct gca ctg ctc 883
 Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro Val Ser Ala Leu Leu
 250 255 260
 cac ggt gaa tac ggt gag gaa gac atc tac atc ggc acc cca gct gtg 931
 His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile Gly Thr Pro Ala Val
 265 270 275
 gtg aac cgc cga ggc atc cgc cgc gtt gtc gaa cta gaa atc acc gac 979
 Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu Leu Glu Ile Thr Asp
 280 285 290
 cac gag atg gaa cgc ttc aag cat tcc gca aat acc ctg cgc gaa att 1027
 His Glu Met Glu Arg Phe Lys His Ser Ala Asn Thr Leu Arg Glu Ile
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<212> PRT

<213> Corynebacterium glutamicum

<400> 130

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His Leu Ala Ile Ile Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val
 35 40 45

Met Asp Leu Asn His Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val
 50 55 60

Thr Lys Gly Thr Tyr Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile
 65 70 75 80

Cys Ala Gly Ala Ala Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val
 85 90 95

Asp Lys Asn Val Lys Ile Met Lys Ser Ile Val Gly Asp Val Met Asp
 100 105 110

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Gly	Ile	Phe	Arg	Arg	Val	Pro	Ala	Ala	Val	Ala	Glu	Pro	Glu	Asn	Val	
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Glu	Gln	Ile	Arg	Asp	Ala	Ile	Ala	Val	Ala	Val	Ala	Arg	Gly	Trp	Ser	
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Val	Val	Gly	Arg	Gly	Gly	Gly	Ser	Ser	Val	Ala	Gly	Asn	Ala	Ile	Gly	
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Glu	Gly	Leu	Ile	Ile	Asp	Thr	Ser	Arg	Tyr	Phe	Asn	Arg	Ile	Leu	Asp	
				90					95					100		
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Ile	Asp	Pro	Val	Ala	Gln	Thr	Ala	Val	Val	Glu	Pro	Gly	Val	Val	Cys	
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Asp	Ala	Leu	Arg	Asp	Ala	Ala	Ala	Glu	Phe	Gly	Leu	Thr	Tyr	Gly	Pro	
		120					125						130			
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Asp	Pro	Ser	Thr	His	Ser	Arg	Cys	Thr	Ile	Gly	Gly	Met	Val	Ala	Asn	
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Asn	Ala	Cys	Gly	Ser	His	Ser	Val	Ala	Phe	Gly	Thr	Ala	Ala	Glu	Asn	
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Leu	Val	Asp	Val	Thr	Leu	Met	Leu	Ser	Asp	Gly	Arg	Glu	Val	Thr	Val	
				170					175					180		
aca	aaa	gat	ggc	tgc	gat	gat	gct	gag	atc	aat	cag	aag	ctc	acc	gac	691
Thr	Lys	Asp	Gly	Cys	Asp	Asp	Ala	Glu	Ile	Asn	Gln	Lys	Leu	Thr	Asp	
			185					190					195			
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Leu	Ala	Ser	Lys	Asn	Gln	Asp	Leu	Ile	Ser	Lys	Glu	Leu	Gly	Arg	Phe	
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Pro	Arg	Gln	Val	Ser	Gly	Tyr	Gly	Leu	His	Tyr	Leu	Ala	His	Asp	Met	
		215				220					225					
gcc	aaa	gca	atg	gcg	ggc	acc	gag	gga	acc	att	gga	atc	att	act	cgg	835
Ala	Lys	Ala	Met	Ala	Gly	Thr	Glu	Gly	Thr	Ile	Gly	Ile	Ile	Thr	Arg	
	230				235					240					245	
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Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val	Lys	Ala	Leu	Ala	Val	
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Gln His Ser Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala
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 Tyr Ser Ser Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala
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 Glu Pro Glu Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val
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Lys	Leu	Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met	Gly	Gly	Asp
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 Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro Ala Ala Ala Phe Asp
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 Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser Ile Thr Arg Ala Arg
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gag	cat	cac	ctg	ctg	ctc	acc	gtc	agc	gag	tcg	cag	aag	gcc	gcg	agc	1315	
Glu	His	His	Leu	Leu	Leu	Thr	Val	Ser	Glu	Ser	Gln	Lys	Ala	Ala	Ser		
390					395					400					405		
gag	aag	atg	ctc	aag	gag	ttc	ttc	gca	gag	ccc	gag	cac	act	ggg	gag	1363	
Glu	Lys	Met	Leu	Lys	Glu	Phe	Phe	Ala	Glu	Pro	Glu	His	Thr	Gly	Glu		
				410					415					420			
ttc	ttc	atc	tgc	acg	tct	gat	gaa	gaa	aag	agc	gcg	tcg	ctc	aac	cgg	1411	
Phe	Phe	Ile	Cys	Thr	Ser	Asp	Glu	Glu	Lys	Ser	Ala	Ser	Leu	Asn	Arg		
			425					430					435				
ttc	ggc	gcg	gcc	agt	gcc	gcc	act	cgc	tac	gcc	gcg	ttg	aag	cgc	cgg	1459	
Phe	Gly	Ala	Ala	Ser	Ala	Ala	Thr	Arg	Tyr	Ala	Ala	Leu	Lys	Arg	Arg		
		440					445					450					
cac	atc	gca	ggg	ctc	atc	ccc	atc	gat	gtg	gcc	ctg	cgt	cgc	gac	gat	1507	
His	Ile	Ala	Gly	Leu	Ile	Pro	Ile	Asp	Val	Ala	Leu	Arg	Arg	Asp	Asp		
	455					460					465						
tgg	aac	tgg	ctc	gag	gtg	ctg	ccg	gag	gag	atc	gac	gac	cag	ctt	gag	1555	
Trp	Asn	Trp	Leu	Glu	Val	Leu	Pro	Glu	Glu	Ile	Asp	Asp	Gln	Leu	Glu		
470					475					480					485		
gtc	aag	gcg	tat	tac	ggg	cac	ttc	ttc	tgc	cat	gtg	atg	cac	cag	gac	1603	
Val	Lys	Ala	Tyr	Tyr	Gly	His	Phe	Phe	Cys	His	Val	Met	His	Gln	Asp		
				490					495					500			
tat	gtc	gcc	aag	cag	ggc	gtg	gat	ctc	gag	gcg	ctg	cac	gac	cgc	atc	1651	
Tyr	Val	Ala	Lys	Gln	Gly	Val	Asp	Leu	Glu	Ala	Leu	His	Asp	Arg	Ile		
			505					510					515				
cag	cac	ctg	ctg	gag	gag	cgc	ggc	gcg	aag	ctg	ccc	gcc	gag	cac	aac	1699	
Gln	His	Leu	Leu	Glu	Glu	Arg	Gly	Ala	Lys	Leu	Pro	Ala	Glu	His	Asn		

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tac ggt cgc atg tac aag ctg ccg gag tcc atg gaa gag cac ttc aag			1747
Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His Phe Lys			
535	540	545	
gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc acg tcg			1795
Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly Thr Ser			
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Pro His Lys Asp Trp Ala			
570			

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<211> 571

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

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Ala Thr Met Pro Phe Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val			
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Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu			
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Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn			
65	70	75	80
Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg			
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Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile			
100	105	110	
Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His			
115	120	125	
Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile			
130	135	140	
Gly Ser Thr Ser Ile Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn			
145	150	155	160
Ser Gly Gly Ser Gln Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala			
165	170	175	
Ile Phe Ala Arg Val Asn Asp Asp Gly Lys Val Glu Leu Val Asn His			
180	185	190	
Leu Gly Ile Ser Leu Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu			
195	200	205	
Gln Arg Gly Glu Trp Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp			

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210					215					220					
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225					230					235					240
Pro	Ala	Arg	Tyr	Asn	Ala	Asn	Pro	Glu	Tyr	Leu	Phe	Glu	Ala	Ser	Gly
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Ser	Ala	Gly	Lys	Leu	Met	Val	Phe	Ala	Val	Arg	Thr	Arg	Thr	Phe	Pro
			260					265					270		
Arg	Glu	Val	His	Pro	Thr	Val	Phe	Tyr	Ile	Gly	Thr	Asn	Asn	Thr	His
		275					280					285			
Glu	Leu	Glu	Glu	Ile	Arg	Arg	Leu	Phe	Leu	Glu	Ala	Asp	Met	Pro	Leu
	290					295					300				
Pro	Ile	Ser	Gly	Glu	Tyr	Met	Gly	Arg	Ser	Ala	Phe	Asp	Leu	Ala	Glu
305					310					315					320
Lys	Tyr	Gly	Lys	Asp	Thr	Phe	Val	Phe	Leu	Lys	Phe	Met	Ser	Pro	Ala
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Leu	Gln	Thr	Arg	Met	Phe	Ser	Phe	Lys	Thr	Trp	Ala	Asn	Gly	Leu	Phe
			340					345					350		
Ser	Lys	Ile	Pro	Gly	Ile	Gly	Pro	Thr	Phe	Ala	Asp	Thr	Val	Ser	Gln
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Ala	Met	Phe	Ser	Val	Leu	Pro	Asn	Gln	Leu	Pro	Lys	Arg	Met	Met	Glu
	370					375					380				
Tyr	Arg	Asn	Arg	Phe	Glu	His	His	Leu	Leu	Leu	Thr	Val	Ser	Glu	Ser
385					390					395					400
Gln	Lys	Ala	Ala	Ser	Glu	Lys	Met	Leu	Lys	Glu	Phe	Phe	Ala	Glu	Pro
				405					410					415	
Glu	His	Thr	Gly	Glu	Phe	Phe	Ile	Cys	Thr	Ser	Asp	Glu	Glu	Lys	Ser
			420					425					430		
Ala	Ser	Leu	Asn	Arg	Phe	Gly	Ala	Ala	Ser	Ala	Ala	Thr	Arg	Tyr	Ala
		435					440					445			
Ala	Leu	Lys	Arg	Arg	His	Ile	Ala	Gly	Leu	Ile	Pro	Ile	Asp	Val	Ala
	450					455					460				
Leu	Arg	Arg	Asp	Asp	Trp	Asn	Trp	Leu	Glu	Val	Leu	Pro	Glu	Glu	Ile
465					470					475					480
Asp	Asp	Gln	Leu	Glu	Val	Lys	Ala	Tyr	Tyr	Gly	His	Phe	Phe	Cys	His
				485					490					495	
Val	Met	His	Gln	Asp	Tyr	Val	Ala	Lys	Gln	Gly	Val	Asp	Leu	Glu	Ala
			500					505					510		
Leu	His	Asp	Arg	Ile	Gln	His	Leu	Leu	Glu	Glu	Arg	Gly	Ala	Lys	Leu
		515					520					525			
Pro	Ala	Glu	His	Asn	Tyr	Gly	Arg	Met	Tyr	Lys	Leu	Pro	Glu	Ser	Met
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cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163
Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
10 15 20

agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259
Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg
 40 45 50

ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac 307
Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp
55 60 65

aac aac ctc atc gtc atc ccg cag gca tcg aac acg ggc ctg act ggt 355
Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly
70 75 80 85

gga tcc ggc ccc ggc ttc caa gac tac gat cgc ccc att gtg atc atc 403
Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile
90 95 100

tgc	act	cac	cgc	atc	gat	gag	gtg	cac	ctc	atc	aac	gac	gcg	cgc	gag	451
Ser	Thr	His	Arg	Ile	Asp	Glu	Val	His	Leu	Ile	Asn	Asp	Ala	Arg	Glu	
			105					110					115			

gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc 499
Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu
120 125 130

gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc 547
Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile
135 140 145

ggc gcc tcg gtc atc ggc ggc atc gcg aac aac tcg ggc ggc agc cag 595
Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln
150 155 160 165

att cgc aag ggt ccg gca ttc acg cgc gaa gcg atc ttc gcc cgc gtc 643
Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val
170 175 180

aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc	691
Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu	
185 190 195	
gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg	739
Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp	
200 205 210	
tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag	787
Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu	
215 220 225	
tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat	835
Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn	
230 235 240 245	
gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg	883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu	
250 255 260	
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Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro	
265 270 275	
acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc	979
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile	
280 285 290	
cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag	1027
Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu Pro Ile Ser Gly Glu	
295 300 305	
tac atg ggc cgc agt gcc ttc gac ttg gcc gag aag tac ggc aaa gac	1075
Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu Lys Tyr Gly Lys Asp	
310 315 320 325	
acc ttc gtc ttc ctg aag ttc atg agt cca gcg ctg cag acg cgc atg	1123
Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala Leu Gln Thr Arg Met	
330 335 340	
ttc tcg ttc aag acg tgg gcc aac ggc ttg ttc tcg aag att ccc ggc	1171
Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe Ser Lys Ile Pro Gly	
345 350 355	
att ggt ccg acc ttc gcc gac acg gta tcg caa gcc atg ttc agc gtg	1219
Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln Ala Met Phe Ser Val	
360 365 370	
ctg ccc aac cag ctg ccc aag cgc atg atg gag tac cgc aac cgt ttc	1267
Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu Tyr Arg Asn Arg Phe	
375 380 385	
gag cat cac ctg ctg ctc acc gtc agc gag tcg cag aag gcc gcg agc	1315
Glu His His Leu Leu Leu Thr Val Ser Glu Ser Gln Lys Ala Ala Ser	
390 395 400 405	
gag aag atg ctc aag gag ttc ttc gca gag ccc gag cac act ggt gag	1363
Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro Glu His Thr Gly Glu	
410 415 420	

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 Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser Ala Ser Leu Asn Arg
 425 430 435

ttc ggc gcg gcc agt gcc gcc act cgc tac gcc gcg ttg aag cgc cgg 1459
 Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala Ala Leu Lys Arg Arg
 440 445 450

cac atc gca ggg ctc atc ccc atc gat gtg gcc ctg cgt cgc gac gat 1507
 His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala Leu Arg Arg Asp Asp
 455 460 465

tgg aac tgg ctc gag gtg ctg ccg gag gag atc gac gac cag ctt gag 1555
 Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile Asp Asp Gln Leu Glu
 470 475 480 485

gtc aag gcg tat tac ggg cac ttc ttc tgc cat gtg atg cac cag gac 1603
 Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His Val Met His Gln Asp
 490 495 500

tat gtc gcc aag cag ggc gtg gat ctc gag gcg ctg cac gac cgc atc 1651
 Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala Leu His Asp Arg Ile
 505 510 515

cag cac ctg ctg gag gag cgc ggc gcg aag ctg ccc gcc gag cac aac 1699
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<211> 533

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

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 20 25 30

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 35 40 45

Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu
 50 55 60

Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn
 65 70 75 80

Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg
 85 90 95

Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile
 100 105 110

Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His
 115 120 125

Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile
 130 135 140

gat cag cag acc aga tgg ctt gat ggt gca aca gtt gcc att gtg gga 499
Asp Gln Gln Thr Arg Trp Leu Asp Gly Ala Thr Val Ala Ile Val Gly
120 125 130

gct ggt gga atc ggt aaa cat ctg gca gcc atg ttg aaa cct ttt ggc 547
Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met Leu Lys Pro Phe Gly
135 140 145

gca aag tct tta gca gta agc agg acc ggt aca ccc acc caa gat ttt 595
Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr Pro Thr Gln Asp Phe
150 155 160 165

gat gca acg gaa cct ata tcc aac ctg cac caa gta ctt gcc gac gcc 643
Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln Val Leu Ala Asp Ala
170 175 180

gac cat gtg gtg ttg tgc gta ccg ctt acc gca gac acc tat cat ctg 691
Asp His Val Val Leu Cys Val Pro Leu Thr Ala Asp Thr Tyr His Leu
185 190 195

atc gga aaa gca gag ctt aaa gca atg cag tcc act gca att ttg atc 739
Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser Thr Ala Ile Leu Ile
200 205 210

aac gtg gct cgc gga gaa gta gta gat aca gaa gca tta gtt gac gcc 787
Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu Ala Leu Val Asp Ala
215 220 225

tta gat gcc caa gaa ata tcc ggg gca ggc tta gat gtc acc gat cct 835
Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu Asp Val Thr Asp Pro
230 235 240 245

gaa cca ttg ccg gac gat cat cca ctg tgg ggg cgc agc aat gtg atc 883
Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly Arg Ser Asn Val Ile
250 255 260

att acc ccg cac gta gcc aac acg ttg acc tcg atg gat cgc atg ctt 931
Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser Met Asp Arg Met Leu
265 270 275

gcc cca gtg gtg gca gaa aac tac cga cgg ttt ctc gct gga gaa aag 979
Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe Leu Ala Gly Glu Lys
280 285 290

atg ctg acc gag gtg gac atc cac aaa ggt tac tagagcagtg gctttgaata 1032
Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
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tag 1035

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<212> PRT
<213> Corynebacterium glutamicum

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Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile
 1 5 10 15

aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg aac ctc ttc ctg 96
 Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu
 20 25 30

cag tac act gac gct cct ggt gca ctg ggt acc gtt ggt acc aag ctg 144
 Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
 35 40 45

ggt gct gct ggc atc aac atc gag gct gct gcg ttg act cag gct gag 192
 Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Leu Thr Gln Ala Glu
 50 55 60

aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag tcc gct gtc tct 240
 Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
 65 70 75 80

gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt gct act tcc ttc 288
 Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
 85 90 95

cag gtt gat ctt gac taattagaga tccatttgct tga 326
 Gln Val Asp Leu Asp
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 <213> Corynebacterium glutamicum

<400> 148
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Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
 35 40 45

Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
 50 55 60

Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
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Gln Val Asp Leu Asp
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Ala	Pro	Thr	Ser	Asn	Ile	His	Ser	Ala	Cys	Glu	His	Ala	Ile	Ser	Leu	
				100					105					110		
Leu	Leu	Ser	Thr	Ala	Arg	Gln	Ile	Leu	Leu	Leu	Met	Arg	Arg	Cys	Val	
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Arg	Ala	Ser	Gly	Ser	Gly	Leu	Leu	Ser	Thr	Val	Trp	Lys	Phe	Ser	Glu	
				130					135					140		
Lys	Leu	Ser	Val	Ser	Ser	Val	Leu	Ala	Thr	Leu	Val	Ser	Cys	Leu	Leu	
				145					150					155		
Ser	Val	Leu	Leu	Arg	Leu	Arg	Pro	Pro	Leu	Leu	Leu	Thr	Ile	Leu	Thr	
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										Met Arg Trp Phe His						
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Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala																
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acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc	211															
Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly																
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agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc	259															
Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe																
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att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc	307															
Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr																
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cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc	355															
His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu																
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Met Gln Lys Asn Ile																115
1 5																
cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt																163
Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser																
10 15 20																
tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att																211
Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile																
25 30 35																
gat. aat ggt att acg tat ttt gat act gca gat att tac gat caa gga																259
Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly																
40 45 50																
gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt																307
Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg																

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att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg				211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val	25	30	35	
gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt				259
Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu	40	45	50	
tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att				307
Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile	55	60	65	
tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag				355
Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys	70	75	80	85
gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg				403
Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu	90	95	100	
cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc				451
His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val	105	110	115	
ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata				499
Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile	120	125	130	
aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc				547
Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val	135	140	145	
act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc				595
Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala	150	155	160	165
gca ctt att acc gca gct act ggc gct gag cct tat tac atc ggc aag				643
Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys	170	175	180	
cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat				691
Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His	185	190	195	
tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa				739
Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys	200	205	210	
tct ggt ttg gaa gcc ggc ctg agc acc gtg ctg gtt cga agc gga att				787
Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile	215	220	225	
tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg				835
Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val	230	235	240	245
atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt				883
Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly	250	255	260	

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Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His	90	95	100	
gcg acg act cgt ttg gct aag tcg tgg agc gtg cgg cct gag gtg gaa				451
Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu	105	110	115	
aac aac aag tca tgg ctg cat gac aat aaa act gtc gct att ttg ggc				499
Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly	120	125	130	
gcc ggt ggc att ggc gtg cgt ctg ctg gaa atg ctc aag ccg ttc aac				547
Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn	135	140	145	
gtg aag acc att gcg gtt aat aac tct ggt cgt ccg gtg gaa ggt gca				595
Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala	150	155	160	165
gat gaa acc ttc gcc atg gat aag gct gag cac gtg tgg gct gag gct				643
Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala	170	175	180	
gat gtg ttt gtg ctc atc ctg ccg ctg act gat gcc act tat cag atc				691
Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile	185	190	195	
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Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val	200	205	210	
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Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala	215	220	225	
ttg aac aac ggc acc att gcg ggt gct gcg ctg gac gtt acc gat cct				835
Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro	230	235	240	245
gag cca ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt				883
Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val	250	255	260	
atc act cct cat act gca aac acg aat gag agg att cgt gct ttg acc				931
Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr	265	270	275	
ggc gaa ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag				979
Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln	280	285	290	
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Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His Ala Thr																
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Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn Val Lys																
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acc att gcg gtt aat aac tct ggt cgt ccg gtg gaa ggt gca gat gaa	345															
Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala Asp Glu																
85 90 95																
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Met Ala Gly Arg Ile 5																
att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg 163																
Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu 20																
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Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln 35																
gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc 259																
Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu 40																
gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg 307																
Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val 55																
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Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala 70																
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Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala 105																
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Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val
      150              155              160

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Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val
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gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg 691
Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val
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Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg
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gat 792

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Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala
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Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp
      65              70              75              80

Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu
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Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met
      100              105              110

Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala
      115              120              125

Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln
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Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg
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Asp Val Ala Val Val Ser His Gly Ala Val Ile Arg Ile Val Ala Thr
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His Ala Thr Gly Val Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly
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 Met Lys Ile Tyr Ala
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cct ttt gct gga atc gtc cac tat ttt gtc gat gaa ggc gat ccc gtg 163
 Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp Glu Gly Asp Pro Val
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 Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr Ile Lys Leu Glu Ala
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 Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala Lys Val Ser Phe Asp
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 Lys Asn
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Trp	Thr	Ala	Gln	Val	Val	Gly	Asp	Asp	Ile	Ala	Trp	Leu	Lys	Leu	Arg		
290						295						300					
Glu	Asp	Gly	Leu	Tyr	Ala	Val	Asn	Pro	Glu	Asn	Gly	Phe	Phe	Gly	Val		
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420						425						430					
Asp	Trp	Glu	His	Gly	Thr	Met	Val	Gly	Ala	Leu	Leu	Ala	Ser	Gly	Gln		
435						440						445					
Thr	Ala	Ala	Ser	Ala	Glu	Ala	Lys	Val	Gly	Thr	Leu	Arg	His	Asp	Pro		
450						455						460					
Met	Ala	Met	Leu	Pro	Phe	Ile	Gly	Tyr	Asn	Ala	Gly	Glu	Tyr	Leu	Gln		
465						470						475					
Asn	Trp	Ile	Asp	Met	Gly	Asn	Lys	Gly	Gly	Asp	Lys	Met	Pro	Ser	Ile		
485						490						495					
Phe	Leu	Val	Asn	Trp	Phe	Arg	Arg	Gly	Glu	Asp	Gly	Arg	Phe	Leu	Trp		
500						505						510					
Pro	Gly	Phe	Gly	Asp	Asn	Ser	Arg	Val	Leu	Lys	Trp	Val	Ile	Asp	Arg		
515						520						525					
Ile	Glu	Gly	His	Val	Gly	Ala	Asp	Glu	Thr	Val	Val	Gly	His	Thr	Ala		
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Lys	Ala	Glu	Asp	Leu	Asp	Leu	Asp	Gly	Leu	Asp	Thr	Pro	Ile	Glu	Asp		
545						550						555					
Val	Lys	Glu	Ala	Leu	Thr	Ala	Pro	Ala	Glu	Gln	Trp	Ala	Asn	Asp	Val		
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Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
170 175 180

aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc 691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe
185 190 195

cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc 739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu
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acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc 787
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His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
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Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
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280 285 290

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295 300 305

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360 365 370

cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga 1267
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cac atg atc aac ttc tagaatccac ctggttgccc ctg 1305

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 Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Val
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 310 315 320 325

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 330 335 340

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Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val	120	125	130	
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Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala	135	140	145	
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Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln	150	155	160	165
gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg				643
Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val	170	175	180	
gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc				691
Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala	185	190	195	
tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg				739
Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser	200	205	210	
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Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu	215	220	225	
ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg				835
Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu	230	235	240	245
gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag				883
Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu	250	255	260	
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Val Cys His Arg Asp Met Lys Val Thr Asp Met Ile Val Ala Leu Met	310	315	320	325
ggc agg tct aag aag gct gag tagtccttagg ttgtaagctt caa				1119
Gly Arg Ser Lys Lys Ala Glu	330			

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Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr
290 295 300

Gln Ala Val Tyr Gly Val Cys His Arg Asp Met Lys Val Thr Asp Met
305 310 315 320

Ile Val Ala Leu Met Gly Arg Ser Lys Lys Ala Glu
325 330

<210> 189

<211> 1015

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> FRXA01025

<400> 189

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ctgaracggt taaatatcgt tttcgaaagg tgggtttcgc gtg gtt tct gta agc 115
Val Val Ser Val Ser
1 5

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163
Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
10 15 20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
25 30 35

agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
40 45 50

acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
55 60 65

gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
70 75 80 85

ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
90 95 100

gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt 451
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser
105 110 115

gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg 499
Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val
120 125 130

ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca 547

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aag caa ccc gac ctg ggg cgc cga ctt gac cca gac aac ctt gat atc 1555
 Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro Asp Asn Leu Asp Ile
 470 475 480 485

gcg gcg cag gcc gtt ttt gct gtc gcc gag gag gcg gcc gtc gac ctg 1603
 Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu Ala Ala Val Asp Leu
 490 495 500

gcg gac gtg ctg gat cgt cgc atc gtg ctc ggc acg ctg ggt tat gtg 1651
 Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly Thr Leu Gly Tyr Val
 505 510 515

caa ccg gct gcc gtg cgt gcg acg gcc gaa gca atg gcg cag gtc acc 1699
 Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala Met Ala Gln Val Thr
 520 525 530

ggg tgg tca gct gag ctt atc gac gcc cag tgc cag tcc tac ctc gcc 1747
 Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys Gln Ser Tyr Leu Ala
 535 540 545

aag caa gac aaa atc caa gcc gtg tta aag ccg tac cgc taacactccg 1796
 Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro Tyr Arg
 550 555 560

tcacgcgacac cgg 1809

<210> 192

<211> 562

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

Met Thr Ser Ala His Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg
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Asp Asn Tyr Asp Val Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln
 20 25 30

Ile Ala Arg His Ala Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu
 35 40 45

Ala Arg Asp Tyr Ser Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile
 50 55 60

His Gly Gly Leu Arg Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln
 65 70 75 80

Glu Ala Val Lys Glu Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu
 85 90 95

Val Ala Pro Arg Ser Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro
 100 105 110

Lys Ala Pro Met Leu Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala
 115 120 125

Trp Gln Arg Asn Gln Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe
 130 135 140

Arg Trp Ile Pro Lys Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp

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145		150		155		160									
Pro	Glu	Gly	Leu	Lys	Gly	Ala	Trp	Arg	His	Asp	Asp	Thr	Leu	Asn	Leu
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His	Ala	Glu	Arg	Leu	Leu	Leu	Ala	Val	Ile	Lys	Ala	Phe	Ala	Ala	Asp
			180					185					190		
Gly	Gly	Thr	Ala	Ile	Asn	His	Ala	Lys	Val	Thr	Arg	Ile	Leu	Arg	Asn
		195					200					205			
Val	Glu	Glu	Gly	Arg	Val	Lys	Gly	Val	Glu	Val	Thr	Asp	Gln	Val	Thr
	210					215					220				
Asn	Thr	Thr	His	Glu	Val	Asn	Ala	Pro	Val	Val	Ile	Asn	Ala	Ala	Gly
225					230					235					240
Pro	Trp	Val	Ala	Gln	Ala	Leu	Gly	Asp	Leu	Ala	Glu	Val	Thr	Lys	Leu
			245						250					255	
Lys	Val	Arg	Gln	Ser	Lys	Gly	Val	His	Leu	Leu	Thr	Gly	Asp	Leu	Gly
			260					265					270		
Ser	Gln	Ser	Gly	Val	Phe	Val	Arg	Gly	Lys	Asn	Gly	Lys	His	Val	Ile
		275					280					285			
Val	Asn	Pro	Trp	Met	Gly	Arg	Thr	Leu	Ile	Gly	Pro	Thr	Asp	Thr	Met
	290					295					300				
Ile	Asp	Gly	Asp	Ala	Asp	Asp	Ala	Ala	Ala	Asp	Glu	Ser	Asp	Ile	Asp
305					310					315					320
Leu	Leu	Leu	Glu	Thr	Ile	Asp	Ser	Val	Arg	Ala	Thr	Pro	Leu	Asp	Arg
			325						330					335	
Lys	Glu	Ile	Ile	Ser	Thr	Leu	Val	Gly	Val	Arg	Pro	Leu	Val	Asp	Asp
			340					345					350		
Gly	Thr	Asp	Thr	Tyr	Thr	Ser	Ser	Arg	Arg	Phe	Asp	Ile	Ser	Asp	His
		355					360					365			
Ala	Asn	Val	Gly	Ile	Asp	Gly	Leu	Val	Ser	Val	Ser	Gly	Gly	Lys	Trp
	370					375					380				
Thr	Thr	Ser	Arg	Val	Met	Gly	Tyr	Lys	Val	Ile	Glu	His	Val	Val	Glu
385					390					395					400
His	Gln	Ala	Ala	Val	Leu	Pro	Pro	Leu	Arg	His	Phe	Asp	Ser	Arg	Gln
				405					410					415	
Met	Pro	Leu	Ser	Thr	Ser	Phe	Gly	Ala	Tyr	Glu	Ser	Val	Ala	Asp	Ser
			420					425					430		
Phe	Glu	Ser	Ala	Leu	Arg	Ser	His	Pro	Glu	Leu	Asp	Val	Asp	Asp	Glu
		435					440					445			
Ile	Arg	Val	His	Leu	Ala	Arg	Leu	Tyr	Gly	Thr	Glu	His	Glu	Lys	Val
	450					455					460				
Leu	Asp	Leu	Val	Ala	Lys	Gln	Pro	Asp	Leu	Gly	Arg	Arg	Leu	Asp	Pro
465					470					475					480

002290 0420960

Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro
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acg gaa gag gat ttt taagatggct ttggttcttg gaa
 Thr Glu Glu Asp Phe
 280

969

<210> 196

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg
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Ile Val Ser Tyr Val Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu
 20 25 30

Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu
 35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg
 50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His
 65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu
 85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu
 100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr
 115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser
 130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp
 145 150 155 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala
 165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val
 180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala
 195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys
 210 215 220

Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp
 225 230 235 240

His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu
 245 250 255

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Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu
260 265 270

Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
275 280

<210> 197

<211> 887

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(864)

<223> RXN01891

<400> 197

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Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr
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tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc cca 96
Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro
20 25 30

gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa gcg 144
Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala
35 40 45

atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac ctt 192
Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu
50 55 60

tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac tct 240
Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser
65 70 75 80

gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca gtt 288
Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val
85 90 95

gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc acc 336
Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr
100 105 110

gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc cag 384
Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln
115 120 125

tcc acc ggt gat ctg tct tgc gtt gcc ggc gct gca agc ttc gac tgg 432
Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp
130 135 140

ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca acc 480
Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
145 150 155 160

ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt cag 528
Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln

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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (7)..(753)

<223> RXA02414

<400> 201

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ggc gcg ttc caa cct gct ggt ggg ccg gtg aag ccg tgg aat aag ccc 99
Gly Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro
                20                      25                      30

gat gcc agc ctg aat cag cag ctg aaa aac aaa tcc cgt gtg cgc aca 147
Asp Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr
                35                      40                      45

ggt ctt acc atc gcc atc ggt tat gta gtg gtg att tgg gcg gtg cat 195
Gly Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His
                50                      55                      60

ttg gca tcc atc gtc att gcg ctg ctc act ggc ttc aac ctg acc aac 243
Leu Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn
                65                      70                      75

ttt ggt att cat ccg ctg gat acc agt gca ctg tgg ggt att ttc acc 291
Phe Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr
                80                      85                      90                      95

tca ccg ctg ttg cat gga agc ttc agc cac ctc att gga aat acc gtt 339
Ser Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val
                100                      105                      110

cca ggc ttt ata ttc agt ttc ctc atc ggt atg agt ggc aag cgc gtg 387
Pro Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val
                115                      120                      125

ttc tgg gaa gtc acg att atc gca ggt ctc atc ggc ggt ctt ggt aca 435
Phe Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr
                130                      135                      140

tgg att ttc ggt gga atc ggc acc aac cac atc ggt gcg tcc ggc ctg 483
Trp Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu
                145                      150                      155

att tat ggc tgg ctt ggc tac ctg atc gtg cgt gga att ttc aac aag 531
Ile Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys
                160                      165                      170                      175

gat att aaa cag ttc ctg ctt ggc ata gtt ttg gcg ttc att tac tcc 579
Asp Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser
                180                      185                      190

ggt ttg ttc tgg ggt ctg cta cct act caa atc ggt gtg tcc tgg cag 627
Gly Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln
                195                      200                      205

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00602740"0622300

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ggc cac ctt ttc ggt gca ctt ggt gga atc ggt gcg ggt gct ttt atc 675
Gly His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile
      210                      215                      220

gcc tcg gat gac ccg gca gcg ttg aaa gcg aag aag caa cag aag aaa 723
Ala Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys
      225                      230                      235

tta gaa aag caa caa cgc caa aga ggc tta tagttttcac ctagcgacta 773
Leu Glu Lys Gln Gln Arg Gln Arg Gly Leu
      240                      245

cac 776

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<210> 202

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr Gly
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Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro Asp
      20                      25                      30

Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr Gly
      35                      40                      45

Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His Leu
      50                      55                      60

Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn Phe
      65                      70                      75                      80

Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr Ser
      85                      90                      95

Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val Pro
      100                      105                      110

Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val Phe
      115                      120                      125

Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr Trp
      130                      135                      140

Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu Ile
      145                      150                      155                      160

Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys Asp
      165                      170                      175

Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser Gly
      180                      185                      190

Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln Gly
      195                      200                      205

His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile Ala

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Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys Leu		
225	230	235 240
Glu Lys Gln Gln Arg Gln Arg Gly Leu		
	245	

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(817)
 <223> RXN01580

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tcaactttgc tccctatcct taaaaagccc acagaaaagg atg tat aag aat atg 115
 Met Tyr Lys Asn Met
 1 5

cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctg gaa aac acc 163
 His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr
 10 15 20

atg acc gct ttc cag gct gcc gcg ccc gct gac gct ttt gag ctg gat 211
 Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp
 25 30 35

atc cac gcc acc gct gac aat cag gtc gtc gtt atc cac gac cgc acc 259
 Ile His Ala Thr Ala Asp Asn Gln Val Val Val Ile His Asp Arg Thr
 40 45 50

gca gcg cgt gtt gcc gcg cca gat tcc ctg cac cgc gac acc ccg gtt 307
 Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His Arg Asp Thr Pro Val
 55 60 65

gcg cgc tta agc gcc gcg caa atc aag gag ata acg ctt atc gac gga 355
 Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile Thr Leu Ile Asp Gly
 70 75 80 85

tcc ccc gta cca acc ctg gag gaa gtt cta ctg cag acg agc ctg ccg 403
 Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu Gln Thr Ser Leu Pro
 90 95 100

atc caa gtg gaa atc aaa tct gcc ggt gca gtt cca gca gcc gca gca 451
 Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val Pro Ala Ala Ala Ala
 105 110 115

tta ttg cag aaa tac cca gag cac ctg gag cgc ctg ctg ttc atc agt 499
 Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg Leu Leu Phe Ile Ser
 120 125 130

ttc atc gat gca gca ctg gtg gaa atc gtg gat cga ctg cca gaa gct 547
 Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp Arg Leu Pro Glu Ala
 135 140 145

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Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp
 145 150 155 160

Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile
 165 170 175

Leu Pro Ser Trp Lys Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His
 180 185 190

Thr Lys Gly Ile Lys Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala
 195 200 205

Phe Gly Ile Ala Gln Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp
 210 215 220

Pro Ser Arg Phe Leu Ala Pro Ser Pro Ala Gly Glu Leu His Trp
 225 230 235

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1291)
 <223> RXA01436

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 cagtagccat cacagcaatt caggcaggag gacgcagcta atg gca ttg gca ctt 115
 Met Ala Leu Ala Leu
 1 5

gtt ttg aac tcc ggt tca tct tcc atc aaa ttc cag ctg gtc aac ccc 163
 Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe Gln Leu Val Asn Pro
 10 15 20

gaa aac tct gcc atc gac gag cca tat gtt tct ggt ctt gtg gag cag 211
 Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser Gly Leu Val Glu Gln
 25 30 35

att ggt gag cca aac ggc cgc atc gta ctc aaa ata gag ggt gaa aaa 259
 Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys Ile Glu Gly Glu Lys
 40 45 50

tat acc cta gag aca ccc atc gca gat cac tcc gaa ggc cta aac ctg 307
 Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser Glu Gly Leu Asn Leu
 55 60 65

gcg ttc gat ctc atg gac cag cac aac tgt ggt cct tcc caa ctg gaa 355
 Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly Pro Ser Gln Leu Glu
 70 75 80 85

atc acc gca gtt gga cac cgc gtg gtc cac ggc gga atc ttg ttc tcc 403
 Ile Thr Ala Val Gly His Arg Val Val His Gly Gly Ile Leu Phe Ser
 90 95 100

gca ccg gaa ctt atc act gat gaa atc gtg gaa atg atc cgc gat ctc 451

002290"0420960

210	215	220
Val Asp Thr Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly 225 230 235 240		
Thr Arg Ser Gly Asp Ile Asp Pro Gly Ile Val Phe His Leu Ser Arg 245 250 255		
Thr Ala Gly Met Ser Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys 260 265 270		
Ser Gly Val Lys Gly Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg 275 280 285		
Glu Met Ile Asp Asn Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile 290 295 300		
Tyr Ile His Gln Leu Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu 305 310 315 320		
Gly Arg Val Asp Thr Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala 325 330 335		
Gln Phe Val Arg Glu Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile 340 345 350		
Glu Ile Asp Pro Glu Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu 355 360 365		
Ile Ser Thr Asp Ala Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn 370 375 380		
Glu Glu Leu Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala 385 390 395		

<210> 207
 <211> 927
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(904)
 <223> RXA00686

<400> 207
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 Met Ala Gly Gly Asn
 1 5
 cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga 163
 Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly
 10 15 20
 gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag 211
 Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu
 25 30 35

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<210> 208
 <211> 268
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 208
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 Ile Ala Val Leu Gly Ala Phe Glu His Thr Met Arg Pro Leu Gly Val
 20 25 30
 Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg
 35 40 45
 Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp
 50 55 60
 Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr
 65 70 75 80
 Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
 85 90 95
 Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
 100 105 110
 Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
 115 120 125
 Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
 130 135 140
 Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
 145 150 155 160
 Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
 165 170 175
 Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
 180 185 190
 His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
 195 200 205
 His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
 210 215 220
 Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
 225 230 235 240
 Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
 245 250 255
 Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr
 260 265

<210> 209
 <211> 1158
 <212> DNA

09602740.062300

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 Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys Leu Glu Leu Ala Arg
 200 205 210

aag cac ggt gcg gaa ttt acc gtg aat gcg cgt aat gaa gat tca ggc 787
 Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg Asn Glu Asp Ser Gly
 215 220 225

gaa gct gta cag aag tac acc aac ggt ggc gca cac ggc gtg ctt gtg 835
 Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala His Gly Val Leu Val
 230 235 240 245

act gca gtt cac gag gca gca ttc ggc cag gca ctg gat atg gct cga 883
 Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala Leu Asp Met Ala Arg
 250 255 260

cgt gca gga aca att gtg ttc aac ggt ctg cca ccg gga gag ttc cca 931
 Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro Pro Gly Glu Phe Pro
 265 270 275

gca tcc gtg ttc aac atc gta ttc aag ggc ctg acc atc cgt gga tcc 979
 Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu Thr Ile Arg Gly Ser
 280 285 290

ctc gtg gga acc cgc caa gac ttg gcc gaa gcg ctc gat ttc ttt gca 1027
 Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala Leu Asp Phe Phe Ala
 295 300 305

cgc gga cta atc aag cca acc gtg agt gag tgc tcc ctc gat gag gtc 1075
 Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys Ser Leu Asp Glu Val
 310 315 320 325

aat ggt gtg ctt gac cgc atg cga aac ggc aag atc gat ggt cgt gtg 1123
 Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys Ile Asp Gly Arg Val
 330 335 340

gcg att cgt ttc taacggattg tgttgaaact gct 1158
 Ala Ile Arg Phe
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<210> 210

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<213> Corynebacterium glutamicum

<400> 210

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Phe Gly His Asp Val Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly
 20 25 30

Pro His Gln Ala Leu Val Lys Val Leu Thr Ser Gly Ile Cys His Thr
 35 40 45

Asp Leu His Ala Leu Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro
 50 55 60

Phe Val Pro Gly His Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro

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<222> (101)..(700)

<223> RXA01571

<400> 211

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cgctcgtagg cgcttttgat ttttcggtag gctaactggg gtg agt atc tca gta 115
Val Ser Ile Ser Val
1 5

aaa gca cta caa aag tcc ggc cca gaa gca cct ttc gag gtc aag atc 163
Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro Phe Glu Val Lys Ile
10 15 20

att gaa cgc cgt gac cca cgc gca gat gat gtg gtt att gat atc aaa 211
Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val Val Ile Asp Ile Lys
25 30 35

gct gcg ggc atc tgc cac agc gat atc cac acc atc cgc aac gaa tgg 259
Ala Ala Gly Ile Cys His Ser Asp Ile His Thr Ile Arg Asn Glu Trp
40 45 50

ggc gag gcg cac ttc ccg ctc acc gtc ggc cac gaa atc gca ggc gtt 307
Gly Glu Ala His Phe Pro Leu Thr Val Gly His Glu Ile Ala Gly Val
55 60 65

gtc tct gcg gtt gga tcc gat gta acc aaa tgg aaa gtc ggc gac cgc 355
Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp Lys Val Gly Asp Arg
70 75 80 85

gtg ggc gtc ggc tgc ctc gtt aac tcc tgc ggc gaa tgc gaa cag tgc 403
Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly Glu Cys Glu Gln Cys
90 95 100

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Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly Asn Val Gly Thr Tyr
105 110 115

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Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln Gly Gly Tyr Ala Glu
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Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser Ile Pro Glu Glu Leu
135 140 145

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Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr
150 155 160 165

tcc cca atc gct cgc tgg aac gtt aaa gaa ggc gac aaa gta gca gtc 643
Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly Asp Lys Val Ala Val
170 175 180

atg ggc ctc ggc ggg act cgg aca cat ggg tgt cca gat cgc tgc agc 691
Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys Pro Asp Arg Cys Ser
185 190 195

caa ggg tgc tgaggttacc gttctgtccc gtt 723
Gln Gly Cys
200

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Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu Ser Arg Ser Leu Arg											20			
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aag gca gaa ctt gcc aag gaa ctc ggc gca gct cgc acg ctt gcg act												211		
Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala Arg Thr Leu Ala Thr											35			
											25	30		
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Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly Glu Phe Asp Phe Ile											50			
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Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp Lys Tyr Leu Ser Leu											65			
											55	60		
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Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys											85			
											70	75	80	
cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc												403		
Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr											100			
											90	95		
gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc												451		
Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe											115			
											105	110		
tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac												499		
Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn												.		
											120	125	130	
gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc												547		
Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe											145			
											135	140		
cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt												592		
Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val														
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<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

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20 25 30

Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly
35 40 45

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gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca 1117
 Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser
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<210> 216

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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 20 25 30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
 35 40 45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
 50 55 60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
 65 70 75 80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
 85 90 95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys
 100 105 110

Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val
 115 120 125

Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu
 130 135 140

Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg
 145 150 155 160

Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly
 165 170 175

Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg
 180 185 190

Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln
 195 200 205

Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln
 210 215 220

Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser
 225 230 235 240

Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly
 245 250 255

006290.0420950

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 Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg Glu Thr Leu Ala Ala
 105 110 115

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 Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr Phe Ala Gly Ala Ile
 120 125 130

cgt gct cag gaa gat cgt tcc tca cag atc gac cac aac act gtt gct 547
 Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp His Asn Thr Val Ala
 135 140 145

tac cac ttc aac gag cca atc ggt gtt gtt ggt cag atc att cct tgg 595
 Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp
 150 155 160 165

aac ttc cca atc ctc atg gct acc tgg aag ctc gca ccg gca ctt gct 643
 Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala
 170 175 180

gca ggt aac gcg atc gtc atg aag cca gct gag cag acc cca gca tcc 691
 Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu Gln Thr Pro Ala Ser
 185 190 195

att ttg tat ctg att aac atc atc ggc gat ctc atc cca gag ggc gtc 739
 Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu Ile Pro Glu Gly Val
 200 205 210

ctc aac atc gtc aac gga ctc ggc ggt gaa gca ggc gct gca ctg tcc 787
 Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala Gly Ala Ala Leu Ser
 215 220 225

ggc tct aat cgg att ggc aag att gct ttc acc ggt tcc acc gag gtc 835
 Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr Gly Ser Thr Glu Val
 230 235 240 245

ggc aag ctg atc aac cgc gct gca tcc gac aag atc att cct gtc acc 883
 Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys Ile Ile Pro Val Thr
 250 255 260

ctg gag ctc ggc ggt aag tcc cca tcc atc ttc ttc tcc gat gtt ctg 931
 Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe Phe Ser Asp Val Leu
 265 270 275

tca cag gat gac gcc ttc gca gag aag gca gtt gaa ggc ttc gcg atg 979
 Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val Glu Gly Phe Ala Met
 280 285 290

ttc gcc ctc aat cag ggt gaa gtt tgt acc tgt cct tcc cgt gca ctt 1027
 Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu
 295 300 305

gtt cat gag tcc atc gct gat gaa ttc ctc gag ctt ggc gtg aag cga 1075
 Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu Leu Gly Val Lys Arg
 310 315 320 325

gtt cag aac atc aag ctg ggt aac cca ctt gat act gaa acc atg atg 1123
 Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp Thr Glu Thr Met Met
 330 335 340

ggt gct cag gcg tcc cag gag cag atg gac aag atc tcc tcc tac ctg 1171

09602740-062300

Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu
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 Arg Ala Leu Ile Leu His Arg Ile Ala Asp Arg Met Glu Glu His Leu
 85 90 95
 Glu Glu Ile Ala Val Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg
 100 105 110
 Glu Thr Leu Ala Ala Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr
 115 120 125
 Phe Ala Gly Ala Ile Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp
 130 135 140
 His Asn Thr Val Ala Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly
 145 150 155 160
 Gln Ile Ile Pro Trp Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu
 165 170 175
 Ala Pro Ala Leu Ala Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu
 180 185 190
 Gln Thr Pro Ala Ser Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu
 195 200 205
 Ile Pro Glu Gly Val Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala
 210 215 220
 Gly Ala Ala Leu Ser Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr
 225 230 235 240
 Gly Ser Thr Glu Val Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys
 245 250 255
 Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe
 260 265 270
 Phe Ser Asp Val Leu Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val
 275 280 285
 Glu Gly Phe Ala Met Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys
 290 295 300
 Pro Ser Arg Ala Leu Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu
 305 310 315 320
 Leu Gly Val Lys Arg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp
 325 330 335
 Thr Glu Thr Met Met Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys
 340 345 350
 Ile Ser Ser Tyr Leu Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu
 355 360 365
 Thr Gly Gly Lys Val Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr
 370 375 380

002290" 0420960

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 Arg Leu Pro Gly Arg Tyr Gly Gln Ser
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Asp	Ala	Val	Ala	Ala	Gly	Pro	Ser	Trp	Ala	Ala	Lys	Thr	Pro	Arg	Glu	
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Gln	Glu	Leu	Ala	Glu	Ile	Ile	His	Leu	Glu	Ala	Gly	Lys	Ser	Asp	Ala	
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Glu	Ala	Leu	Gly	Glu	Val	Ala	Tyr	Gly	Ala	Glu	Tyr	Phe	Arg	Trp	Phe	
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<212> DNA
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<222> (101)..(724)
<223> RXN03150
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Val Glu Ala Gln Phe
1 5
acc tct ccc ctg ctc aac aat ggg caa acc tgt ttc ctt ggt acc cga 163
Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys Phe Leu Gly Thr Arg
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Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val Val Asp Ala Phe Thr

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gaa	gcc	gca	gac	ctc	gac	gaa	gcc	gta	tcc	ggc	gcc	atc	gcc	gca	aaa	288
Glu	Ala	Ala	Asp	Leu	Asp	Glu	Ala	Val	Ser	Gly	Ala	Ile	Ala	Ala	Lys	
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ctc	cgc	aac	gcc	ggc	caa	gta	tgc	atc	gca	gct	aac	cgt	ttc	ttg	gtt	336
Leu	Arg	Asn	Ala	Gly	Gln	Val	Cys	Ile	Ala	Ala	Asn	Arg	Phe	Leu	Val	
			100				105						110			
cat	gaa	tcc	cgc	gct	gcc	gaa	ttc	acc	tca	aag	ctg	gcg	aca	gcc	atg	384
His	Glu	Ser	Arg	Ala	Ala	Glu	Phe	Thr	Ser	Lys	Leu	Ala	Thr	Ala	Met	
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Gln	Asn	Thr	Pro	Ile	Gly	Pro	Val	Ile	Ser	Ala	Arg	Gln	Arg	Asp	Arg	
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Ile	Ala	Ala	Leu	Val	Asp	Glu	Ala	Ile	Thr	Asp	Gly	Ala	Arg	Leu	Ile	
	145				150					155					160	
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Ile	Gly	Gly	Glu	Val	Pro	Asp	Gly	Ser	Gly	Phe	Phe	Tyr	Pro	Ala	Thr	
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Ile	Leu	Ala	Asp	Val	Pro	Ala	Gln	Ser	Arg	Ile	Val	His	Glu	Glu	Ile	
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Phe	Gly	Pro	Val	Ala	Thr	Ile	Ala	Thr	Phe	Thr	Asp	Leu	Ala	Glu	Gly	
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Ser	Asn	Asn	Val	Lys	Ala	Thr	Gln	Tyr	Met	Ala	Glu	His	Leu	Glu	Ala	
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Gly	Met	Val	Gly	Ile	Asn	Arg	Gly	Ala	Ile	Ser	Asp	Pro	Ala	Ala	Pro	
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Phe	Gly	Gly	Ile	Gly	Gln	Ser	Gly	Phe	Gly	Arg	Glu	Gly	Gly	Thr	Glu	
			260				265						270			
gga	atc	gaa	gaa	tat	ctc	tcc	gtg	cgt	tac	ctc	gct	ttg	ccg			858
Gly	Ile	Glu	Glu	Tyr	Leu	Ser	Val	Arg	Tyr	Leu	Ala	Leu	Pro			
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002290"0420960


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<223> RXN01498
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Val	His	Leu	Leu	Ile	Glu	Ala	Gly	Leu	Pro	Arg	Asp	Leu	Met	Gln	Val	
		200					205					210				
gtc	acc	ggc	cct	ggc	gat	att	gtt	ggc	ggg	gag	att	gca	gct	cag	tgt	787
Val	Thr	Gly	Pro	Gly	Asp	Ile	Val	Gly	Gly	Ala	Ile	Ala	Ala	Gln	Cys	
	215					220					225					
gat	ttc	ctc	atg	ttc	act	gga	tcc	acg	gcc	acg	ggc	cgg	atc	ttg	ggg	835
Asp	Phe	Leu	Met	Phe	Thr	Gly	Ser	Thr	Ala	Thr	Gly	Arg	Ile	Leu	Gly	
230					235					240					245	
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Arg	Thr	Met	Gly	Glu	Arg	Leu	Val	Gly	Phe	Ser	Ala	Glu	Leu	Gly	Gly	
			250						255					260		
aag	aac	cct	ctt	att	gtg	gcc	aag	gat	gca	gat	ctg	gac	aag	gtg	gaa	931
Lys	Asn	Pro	Leu	Ile	Val	Ala	Lys	Asp	Ala	Asp	Leu	Asp	Lys	Val	Glu	
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tcc	act	gaa	cgt	att	tat	gtc	gag	gaa	gac	gtg	tac	gag	gag	gtg	att	1027
Ser	Thr	Glu	Arg	Ile	Tyr	Val	Glu	Glu	Asp	Val	Tyr	Glu	Glu	Val	Ile	
	295					300					305					
gca	cgg	ttt	agc	aag	gag	gag	aaa	gcc	atg	tcc	att	ggg	gcc	gga	ttt	1075
Ala	Arg	Phe	Ser	Lys	Ala	Ala	Lys	Ala	Met	Ser	Ile	Gly	Ala	Gly	Phe	
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Glu	Trp	Lys	Tyr	Glu	Met	Gly	Ser	Leu	Ile	Asn	His	Ala	Gln	Leu	Asp	
				330					335					340		
cgg	gtg	agc	acc	ttt	gtt	gat	cag	gct	aaa	gct	gag	ggc	gcc	acg	gtg	1171
Arg	Val	Ser	Thr	Phe	Val	Asp	Gln	Ala	Lys	Ala	Ala	Gly	Ala	Thr	Val	
			345					350					355			
ctg	tgc	ggg	ggc	aag	tca	cgc	cct	gat	att	ggg	ccc	ttc	ttc	tat	gag	1219
Leu	Cys	Gly	Gly	Lys	Ser	Arg	Pro	Asp	Ile	Gly	Pro	Phe	Phe	Tyr	Glu	
		360					365					370				
ccc	acg	gta	ttg	gag	gat	gtc	cca	gag	ggc	acc	cca	ctg	ctc	acg	gag	1267
Pro	Thr	Val	Leu	Ala	Asp	Val	Pro	Glu	Gly	Thr	Pro	Leu	Leu	Thr	Glu	
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gaa	gtc	ttc	ggg	ccg	gtg	gtg	ttc	atc	gaa	aag	gta	gcc	aca	ctg	gaa	1315
Glu	Val	Phe	Gly	Pro	Val	Val	Phe	Ile	Glu	Lys	Val	Ala	Thr	Leu	Glu	
390					395					400					405	
gaa	gcc	gtc	gat	aag	gca	aat	ggc	acg	ccc	tac	ggc	ctg	aat	gag	tcc	1363
Glu	Ala	Val	Asp	Lys	Ala	Asn	Gly	Thr	Pro	Tyr	Gly	Leu	Asn	Ala	Ser	
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 165 170 175
 Leu Ala Gly Asn Ala Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe
 180 185 190
 Ser Cys Leu Ile Met Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg
 195 200 205
 Asp Leu Met Gln Val Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala
 210 215 220
 Ile Ala Ala Gln Cys Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr
 225 230 235 240
 Gly Arg Ile Leu Gly Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser
 245 250 255
 Ala Glu Leu Gly Gly Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp
 260 265 270
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 275 280 285
 Gly Gln Leu Cys Val Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val
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 Tyr Glu Glu Val Ile Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser
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 Ile Gly Ala Gly Phe Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn
 325 330 335
 His Ala Gln Leu Asp Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala
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 Pro Phe Phe Tyr Glu Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr
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 Val Ala Thr Leu Glu Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr
 405 410 415
 Gly Leu Asn Ala Ser Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val
 420 425 430
 Ala Gly Gln Leu Glu Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala
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 Ala Thr Trp Ala Ser Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser
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 Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu Ala His Ala Ala Glu
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 410 415 420

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 Val His Ile Asn Asp Leu Thr Val Asn Asp Glu Pro His Val Met Phe
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 Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe Asn Gly Asp Trp Ala
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atc gag gag ttc acc aca gat cga tgg atc ggc atc aag cgc agc 1552
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 35 40 45

Asp Val Asp Ala Ala Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp
 50 55 60

Ala Ala Thr Pro Ala Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala
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Glu Leu Leu Glu Glu His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys
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Glu Ser Gly Ser Thr Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala
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Gly Asn Ile Thr Lys Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly
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 <223> RXN00868

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 Met Ala Glu Thr Lys
 1 5
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 Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe Leu Gly His Gln Trp
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 Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile Pro Gly Met Phe Gly
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 Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly Gln Ala Leu Lys Gln
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 Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr Tyr Gln Ala Arg Asn
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 gag cag gcg atg gtg cac cag tct gtt gga tat gca cgc atg cac cgc 355
 Glu Gln Ala Met Val His Gln Ser Val Gly Tyr Ala Arg Met His Arg
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 cgt cgt ggc aca tac gca tct gcc gca tct gtt gga ccc ggc gcg acc 403
 Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val Gly Pro Gly Ala Thr
 90 95 100
 aac ctg tta acc ggt gcg gct ctt gct acc acc aac cgt ttg cca gcg 451
 Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr Asn Arg Leu Pro Ala
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 ttg ctg ctg cct agt gat act ttt gcc acc cgc gtg gcg gat cca gtg 499
 Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg Val Ala Asp Pro Val
 120 125 130
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cag ttg ttc tct att gcg ttg gct gcg atg cgt gtg ttg act gat ccc 643
 Gln Leu Phe Ser Ile Ala Leu Ala Met Arg Val Leu Thr Asp Pro
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gca gaa acc ggt gcg gtc acc att gcg ctt cca gaa gat gtg cag gct 691
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 185 190 195

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 Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln Asp Arg Glu Trp His
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 Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu Ala Arg Ala Ile Glu
 215 220 225

gtc atc aaa aac gct aag aat ccg atg atc att gct ggt ggc gga gtg 835
 Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile Ala Gly Gly Gly Val
 230 235 240 245

ttg tac tcc gat gcg gaa acg cag ctg cag gca ctt gtg gag cag act 883
 Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala Leu Val Glu Gln Thr
 250 255 260

ggc att cca gtg ggt acc tcc caa gct ggt ggt ggc gtg ttg gcg tgg 931
 Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly Gly Val Leu Ala Trp
 265 270 275

gat cat gca caa aac tta ggt ggt gtg ggt gcc acc gga acg ttg gct 979
 Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala Thr Gly Thr Leu Ala
 280 285 290

gcc aac cgc att gcg ggt gat gct gat gtg atc atc ggt atc ggt act 1027
 Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile Ile Gly Ile Gly Thr
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cgt tac agc gat ttc acc acc gca tct cgc act gcg ttc caa aac cct 1075
 Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr Ala Phe Gln Asn Pro
 310 315 320 325

gat gtc acc ttc atc aac atc aat gtt gct tcc ttc gat gct tac aag 1123
 Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser Phe Asp Ala Tyr Lys
 330 335 340

cat ggc act cag ttg cct gtg att gca gat gca cgc gag gca att gtg 1171
 His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala Arg Glu Ala Ile Val
 345 350 355

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 Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val Ala Glu Asp Tyr Ala
 360 365 370

cag cgc atc gcg aag gaa aag gct gcg tgg gac gca gaa gta gat aag 1267
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Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
 50              55              60

Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
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Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
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Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
115              120              125

Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
130              135              140

Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
145              150              155              160

Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
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Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val
180              185              190

Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp
195              200              205

Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr
210              215              220

Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn
225              230              235              240

Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu
245              250              255

Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro
260              265              270

Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val
275              280              285

Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile
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 Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys Asp Val Gln Asn Ala
 150 155 160 165

gaa ttg gat ttc gtc tgg cca cca aag atc gac ctg cca ggc tac cgc 643
 Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp Leu Pro Gly Tyr Arg
 170 175 180

cca gtt tca aca cca cat gct cgc cag atc gag cag gca gtc aag ctg 691
 Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu Gln Ala Val Lys Leu
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 Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val Gly Gly Gly Val Ile
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aag gct gac gca cac gaa gag ctt cgt gcg ttc gct gag tac acc ggc 787
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 Ile Pro
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 35 40 45

Gln Gly Ala Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg
 50 55 60

Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
 65 70 75 80

Thr Pro Ile Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
 85 90 95

Thr Gly Gln Val Gly Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu
 100 105 110

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<223> RXA02474
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Met Ser Lys Val Ala 5																
atg gtt acc ggt ggt gca caa ggc atc ggt cgt gga att tca gag aag 163																
Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg Gly Ile Ser Glu Lys 20																
ctg gca gca gat ggt ttc gat att gcc gta gcc gac ctg cca caa cag 211																
Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala Asp Leu Pro Gln Gln 35																
gaa gaa caa gct gca gag acc atc aag ttg att gaa gct gca ggt caa 259																
Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile Glu Ala Ala Gly Gln 50																
aag gct gta ttc gtt gga tta gat gtc acc gat aag gct aat ttc gac 307																
Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp Lys Ala Asn Phe Asp 65																
agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta 355																
Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu 85																
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Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys 130																
ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca 547																
Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro 145																
atc ttg agc gcc tac tcc acc acc aaa ttc gcg gtt cgt ggc ctc acc 595																
Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr 165																
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				Met	Lys	Ser	Ile	Phe								
				1				5								
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Ile	Ser	Gly	Ala	Ala	Asn	Gly	Ile	Gly	Lys	Ala	Val	Ala	Leu	Lys	Phe	
				10				15						20		
ctt	cac	gaa	ggt	tgg	ctc	gtt	gga	gcc	tac	gac	ctc	gcg	gaa	atc	acc	211
Leu	His	Glu	Gly	Trp	Leu	Val	Gly	Ala	Tyr	Asp	Leu	Ala	Glu	Ile	Thr	
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tac	tca	cac	ccc	aat	ctt	cgc	tgg	ggc	tac	ctc	aat	gtt	cga	cag	tcc	259
Tyr	Ser	His	Pro	Asn	Leu	Arg	Trp	Gly	Tyr	Leu	Asn	Val	Arg	Gln	Ser	
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Glu	Ser	Trp	Asp	Lys	Ala	Leu	Glu	Asp	Phe	Ala	Thr	His	Thr	Gly	Gly	
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Thr	Ile	Asp	Val	Val	Asp	Asn	Asn	Ala	Gly	Val	Ile	Ile	Glu	Gly	Pro	
	70				75					80					85	
ctg	cag	gac	gca	gag	gag	ggg	agc	gtc	gac	aag	ctt	ctt	gca	atc	aac	403
Leu	Gln	Asp	Ala	Glu	Glu	Gly	Ser	Val	Asp	Lys	Leu	Leu	Ala	Ile	Asn	
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gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca 1075
 Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser
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 35 40 45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
 50 55 60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
 65 70 75 80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
 85 90 95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys
 100 105 110

Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val
 115 120 125

Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu
 130 135 140

Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg
 145 150 155 160

Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly
 165 170 175

Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg
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Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln

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 35 40 45
 Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu
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 Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr
 65 70 75 80
 Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn
 85 90 95
 Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe
 100 105 110
 Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile
 115 120 125
 Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile
 130 135 140
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 Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys
 165 170 175
 Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val
 180 185 190
 Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu
 195 200 205
 Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
 210 215 220
 Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile
 225 230 235 240
 Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
 245 250 255
 Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu
 260 265 270
 Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln
 275 280 285
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 Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His Gly Asp Thr Leu Ser
 295 300 305

aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt gag gct ctg 1075
 Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser Gln Leu Glu Ala Leu
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ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc gag ggt gtg 1123
 Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr Glu Gly Val
 330 335 340

gac aag ttc gtt gct tct tgg agc gaa ctg ctt gag tcc atg gaa gct 1171
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 Arg Leu Lys
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 35 40 45

Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
 50 55 60

Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
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Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
 85 90 95

Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
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Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
 115 120 125

Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
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 180 185 190
 Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val
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 Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala
 210 215 220
 Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val
 225 230 235 240
 Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr
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 Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala
 260 265 270
 Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr
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 Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His
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 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
 305 310 315 320
 Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
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 Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu
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 Glu Ser Met Glu Ala Arg Leu Lys
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 Leu Thr Thr Leu Thr
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ctg tca cct gaa ctt cag gcg ctc act gta cgc aat tac ccc tct gat 163

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Trp	Ser	Asp	Val	Asp	Thr	Lys	Ala	Val	Asp	Thr	Val	Arg	Val	Leu	Ala	
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gca	gac	gct	gta	gaa	aac	tgt	ggc	tcc	ggc	cac	cca	ggc	acc	gca	atg	259
Ala	Asp	Ala	Val	Glu	Asn	Cys	Gly	Ser	Gly	His	Pro	Gly	Thr	Ala	Met	
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Ser	Leu	Ala	Pro	Leu	Ala	Tyr	Thr	Leu	Tyr	Gln	Arg	Val	Met	Asn	Val	
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Asp	Pro	Gln	Asp	Thr	Asn	Trp	Ala	Gly	Arg	Asp	Arg	Phe	Val	Leu	Ser	
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Cys	Gly	His	Ser	Ser	Leu	Thr	Gln	Tyr	Ile	Gln	Leu	Tyr	Leu	Gly	Gly	
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ttc	ggc	ctt	gag	atg	gat	gac	ctg	aag	gct	ctg	cgc	acc	tgg	gat	tcc	451
Phe	Gly	Leu	Glu	Met	Asp	Asp	Leu	Lys	Ala	Leu	Arg	Thr	Trp	Asp	Ser	
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Leu	Thr	Pro	Gly	His	Pro	Glu	Tyr	Arg	His	Thr	Lys	Gly	Val	Glu	Ile	
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Thr	Thr	Gly	Pro	Leu	Gly	Gln	Gly	Leu	Ala	Ser	Ala	Val	Gly	Met	Ala	
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atg	gct	gct	cgt	cgt	gag	cgt	ggc	cta	ttc	gac	cca	acc	gct	gct	gag	595
Met	Ala	Ala	Arg	Arg	Glu	Arg	Gly	Leu	Phe	Asp	Pro	Thr	Ala	Ala	Glu	
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ggc	gaa	tcc	cca	ttc	gac	cac	cac	atc	tac	gtc	att	gct	tct	gat	ggg	643
Gly	Glu	Ser	Pro	Phe	Asp	His	His	Ile	Tyr	Val	Ile	Ala	Ser	Asp	Gly	
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gac	ctg	cag	gaa	ggg	gtc	acc	tct	gag	gca	tcc	tcc	atc	gct	ggc	acc	691
Asp	Leu	Gln	Glu	Gly	Val	Thr	Ser	Glu	Ala	Ser	Ser	Ile	Ala	Gly	Thr	
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cag	cag	ctg	ggc	aac	ctc	atc	gtg	ttc	tgg	gat	gac	aac	cgc	atc	tcc	739
Gln	Gln	Leu	Gly	Asn	Leu	Ile	Val	Phe	Trp	Asp	Asp	Asn	Arg	Ile	Ser	
		200					205						210			
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Ile	Glu	Asp	Asn	Thr	Glu	Ile	Ala	Phe	Asn	Glu	Asp	Val	Val	Ala	Arg	
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tac	aag	gct	tac	ggc	tgg	cag	acc	att	gag	gtt	gag	gct	ggc	gag	gac	835
Tyr	Lys	Ala	Tyr	Gly	Trp	Gln	Thr	Ile	Glu	Val	Glu	Ala	Gly	Glu	Asp	
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<213> Corynebacterium glutamicum

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Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp	65	70	75
Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln	85	90	95
Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu	100	105	110
Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr	115	120	125
Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser	130	135	140
Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp	145	150	155
Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val	165	170	175
Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser	180	185	190
Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp	195	200	205
Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu	210	215	220
Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val	225	230	235
Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala	245	250	255
Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile	260	265	270
Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala	275	280	285
Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe	290	295	300
Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr	305	310	315
Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val	325	330	335

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Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe
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 Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu
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 Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser
 370 375 380
 Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly
 385 390 395 400
 Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser
 405 410 415
 Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu
 420 425 430
 Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly
 435 440 445
 Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly
 450 455 460
 Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu
 465 470 475 480
 Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser
 485 490 495
 Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu
 500 505 510
 Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp
 515 520 525
 Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu
 530 535 540
 Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu
 545 550 555 560
 Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val
 565 570 575
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 580 585 590
 Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala
 595 600 605
 Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met Asp Trp Phe
 610 615 620
 Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val
 625 630 635 640
 Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg
 645 650 655

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Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala
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 Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala Arg Leu Gly
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aca tcc cac tac tcc cgt cag ctc tcc ctc gtg gac aac gct gag ttc 152
 Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn Ala Glu Phe
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ggc gag cat tcc ctg cta gaa ggg tgg act cgt tcc cac ctc att gcc 200
 Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His Leu Ile Ala
 40 45 50

cac gtg gca tac aac gcc atc gca ctg tgc aac ctc atg cac tgg gca 248
 His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met His Trp Ala
 55 60 65

aat act ggt gag gaa acc cca atg tac gtg tgc cca gaa gcg cgc aac 296
 Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu Ala Arg Asn
 70 75 80

gag gaa att gcc tac ggt tcc acg ctc aat ccc gat gcg ttg cgt aac 344
 Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala Leu Arg Asn
 85 90 95

ctg cat gaa cac tcc gtc gca cgc ctg gac gtg gct tgg cgt gaa acg 392
 Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp Arg Glu Thr
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tct gaa gat gct tgg tca cac gag gtt ctg aca gct cag gga cgc act 440
 Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln Gly Arg Thr
 120 125 130

gtc cca gct agt gaa aca ttg tgg atg cgt tcc cgc gaa gtc tgg atc 488
 Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu Val Trp Ile
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 His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp Ile Pro Glu
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gtc atc ctg cgc acc tta gct gca gaa atc aca caa aag tgg aca agc 584
 Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys Trp Thr Ser
 165 170 175

caa gga gcc ggc gag gga ctt gtg ctt ctc gac gag ccc tcc agc act 632
 Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro Ser Ser Thr
 180 185 190 195

cgc tac ccc gcc gcc cca ggg cag gac gag gta gta gtg tcc ggt agc 680
 Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val Ser Gly Ser
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ctt gca ggc att gtt cgc tac gcc gct ggc cgc ggt tcc gat gga gtc 728
 Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser Asp Gly Val
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act tct tcc act gga gag gtt cca gag cca ccg cgc tgg ctg 770
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Ala Glu Phe Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His
 35 40 45

Leu Ile Ala His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met
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His Trp Ala Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu
 65 70 75 80

Ala Arg Asn Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala
 85 90 95

Leu Arg Asn Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp
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Arg Glu Thr Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln
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Gly Arg Thr Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu
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Met Thr Asn Gly Asp															5
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Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn															20
10 15															
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Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn															35
25 30															
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Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu															50
40 45															
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Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu															65
55 60															
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Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr															85
70 75 80															
gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc															403
Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile															100
90 95 100															

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 Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys
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 atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
 375 380 385
 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
 390 395 400 405
 ctc ggc gac ctc atc gat tca tgg cgt cgc gtc att gtc acc gcc acc 1363
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
 410 415 420
 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
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 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
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 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
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<213> Corynebacterium glutamicum

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 Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
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 Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met

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Thr	Ile	Arg	Arg	Glu	Lys	Glu	Ile	Ser	Ala	Arg	Gly	Leu	His	Phe	Val		
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Gly	Ala	Gly	Ile	Ser	Gly	Gly	Glu	Glu	Gly	Ala	Leu	Asn	Gly	Pro	Ser		
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Ile	Gly	Pro	Asp	Gly	Ala	Gly	His	Phe	Val	Lys	Met	Val	His	Asn	Gly		
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Ile	Glu	Tyr	Ala	Asp	Met	Gln	Val	Ile	Gly	Glu	Ala	Tyr	His	Leu	Leu		
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Arg	Tyr	Ala	Ala	Gly	Met	Gln	Pro	Ala	Glu	Ile	Ala	Glu	Val	Phe	Lys		
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Glu	Trp	Asn	Ala	Gly	Asp	Leu	Asp	Ser	Tyr	Leu	Ile	Glu	Ile	Thr	Ala		
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Glu	Val	Leu	Ser	Gln	Val	Asp	Ala	Glu	Thr	Gly	Lys	Pro	Leu	Ile	Asp		
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Ser	Lys	Leu	Val	Ala	Tyr	Ala	Gln	Gly	Phe	Asp	Glu	Ile	Lys	Ala	Gly		
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Ser	Asp	Glu	Asn	Asn	Trp	Asp	Val	Asp	Pro	Arg	Asp	Leu	Ala	Thr	Ile		
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Trp	Arg	Gly	Gly	Cys	Ile	Ile	Arg	Ala	Lys	Phe	Leu	Asn	Arg	Ile	Val		
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Glu	Ala	Tyr	Asp	Ala	Asn	Ala	Glu	Leu	Glu	Ser	Leu	Leu	Leu	Asp	Pro		
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Tyr	Phe	Lys	Ser	Glu	Leu	Gly	Asp	Leu	Ile	Asp	Ser	Trp	Arg	Arg	Val		
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Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly	
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cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct	595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala	
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Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly	
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Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp	
185 190 195	
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc	739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly	
200 205 210	
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Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly	
215 220 225	
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag	835
Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln	
230 235 240 245	
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct	883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala	
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gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat	931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp	
265 270 275	
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca	979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala	
280 285 290	
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Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro	
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Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln	
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Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala	
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Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn	
345 350 355	

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Ile	Gly	Pro	Asp	Gly	Ala	Gly	His	Phe	Val	Lys	Met	Val	His	Asn	Gly	
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Ile	Glu	Tyr	Ala	Asp	Met	Gln	Val	Ile	Gly	Glu	Ala	Tyr	His	Leu	Leu	
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Arg	Tyr	Ala	Ala	Gly	Met	Gln	Pro	Ala	Glu	Ile	Ala	Glu	Val	Phe	Lys	
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Glu	Trp	Asn	Ala	Gly	Asp	Leu	Asp	Ser	Tyr	Leu	Ile	Glu	Ile	Thr	Ala	
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Glu	Val	Leu	Ser	Gln	Val	Asp	Ala	Glu	Thr	Gly	Lys	Pro	Leu	Ile	Asp	
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Val	Ile	Val	Asp	Ala	Ala	Gly	Gln	Lys	Gly	Thr	Gly	Arg	Trp	Thr	Val	
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Lys	Ala	Ala	Leu	Asp	Leu	Gly	Ile	Ala	Thr	Thr	Gly	Ile	Gly	Glu	Ala	
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Val	Phe	Ala	Arg	Ala	Leu	Ser	Gly	Ala	Thr	Ser	Gln	Arg	Ala	Ala	Ala	
	290					295					300					
Gln	Gly	Asn	Leu	Pro	Ala	Gly	Val	Leu	Thr	Asp	Leu	Glu	Ala	Leu	Gly	
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Val	Asp	Lys	Ala	Gln	Phe	Val	Glu	Asp	Val	Arg	Arg	Ala	Leu	Tyr	Ala	
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Ser	Lys	Leu	Val	Ala	Tyr	Ala	Gln	Gly	Phe	Asp	Glu	Ile	Lys	Ala	Gly	
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Trp	Arg	Gly	Gly	Cys	Ile	Ile	Arg	Ala	Lys	Phe	Leu	Asn	Arg	Ile	Val	
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Glu	Ala	Tyr	Asp	Ala	Asn	Ala	Glu	Leu	Glu	Ser	Leu	Leu	Leu	Asp	Pro	
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 20 25 30

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 35 40 45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
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Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65 70 75 80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
 85 90 95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
 100 105 110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
 115 120 125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
 130 135 140

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
 145 150 155 160

Thr Ala Lys Gln Trp Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn
 165 170 175

Ile Thr Arg Leu Pro Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn
 180 185 190

Asp Thr Tyr Glu Gly Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu
 195 200 205

Lys Met Ala Glu His Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp
 210 215 220

Phe Asp Val Arg Asp Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val
 225 230 235 240

Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys
 245 250 255

Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly

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260 265 270
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 275 280 285
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 Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe
 305 310 315 320
 Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp
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 Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala
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 Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu
 355 360 365
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<212> DNA

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<222> (1)..(489)

<223> FRXA02596

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 Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
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acc ggt gac ttc caa gga acc cca gtg atg aac tac aac gat gcg gac 144
 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
 35 40 45

gta cct ttc acc cgc atc cac gag ttc cgt cac ttc cac cca gag cgt 192
 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
 50 55 60

gat gac agt tac ccc aag gat aag acc gtc atc atg cgc gag ttc tcc 240
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Arg Gly His

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Met Thr Glu Ser Lys
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aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
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gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
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Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
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Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser
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Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly
70 75 80 85

tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403
Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe
90 95 100

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Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser
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cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499
Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp
120 125 130

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Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly
135 140 145

cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595
Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp
150 155 160 165

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gcg ggc ctg gga ttc ggt ggc ggt tgt ttg cct aaa gac atc cgc gct 144
Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala
35 40 45

ttc atg gca cgc gcg ggc gaa ttg ggt gct gac cag gca tta acg ttc 192
Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe
50 55 60

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Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val
65 70 75 80

cag ctg gcc aaa gag atg tgt ggc ggt tcg ctg ctg ggc aag cgg gtt 288
Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val
85 90 95

aca gtg ctc ggc gcc gca ttc aaa ccc aac tcg gac gat gtc cgc gat 336
Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp
100 105 110

tct ccg gcg ctg tcg gtc gcg ggt tcg ctg tcg ctc cag ggt gcg gcg 384
Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala
115 120 125

gtc tcg gtc tac gac ccg gaa gct atg gac aac gct cga cgc gtc ttc 432
Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe
130 135 140

ccg acg ctc agc tat gcg tcc agc act aaa gag gcg ctt atc gac gcc 480
Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala
145 150 155 160

cac ctc gtc gtt ctt gcc act gaa tgg caa gaa ttc cgc gac ctt gac 528
His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp
165 170 175

ccc gaa gtg gcg gga ggg gtc gtc gag aag cgc gct att att gat ggc 576
Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly
180 185 190

cga aac gtc ctc gat gtt gcc aaa tgg aag gcc gcc ggt tgg gaa atg 624
Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met
195 200 205

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210 215

<210> 262

<211> 215

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

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 Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala
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 Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe
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 Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val
 65 70 75 80
 Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val
 85 90 95
 Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp
 100 105 110
 Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala
 115 120 125
 Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe
 130 135 140
 Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala
 145 150 155 160
 His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp
 165 170 175
 Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly
 180 185 190
 Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met
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 Glu Ala Leu Gly Arg Asn Leu
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1201)

<223> RXA02485

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tacgcgttgc catgaggata agactaccgt tagtggggtg ttg gat tca tcg cta 115
 Leu Asp Ser Ser Leu
 1 5

gcc cag gaa atc gcc gcg atc gac ggc gtc gaa ctc gat tcg gaa gtc 163
 Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu Leu Asp Ser Glu Val
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 Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly Gly Lys Pro Arg Ser
 25 30 35

gcc gta cgt tgc cag acc acg gag gcg ctg gtc agc gcc ata aaa ttg 259
 Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val Ser Ala Ile Lys Leu
 40 45 50

ctt gac gac gcc tcc ctc ccc ctc ctc att gtc ggc ggc ggg tcc aat 307
 Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val Gly Gly Gly Ser Asn
 55 60 65

ctc gtc gtg gcc gac ggc gat ctg gat gtt att gcc gtc atc atc gaa 355
 Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile Ala Val Ile Ile Glu
 70 75 80 85

acc gac gac gtc tcc atc aac ctc acc gac ggt ctc ctc acc gcc gat 403
 Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly Leu Leu Thr Ala Asp
 90 95 100

gca ggc gct gtt tgg gac gat gtt gtc cac ctt tcg gtg gat gcc ggc 451
 Ala Gly Ala Val Trp Asp Asp Val Val His Leu Ser Val Asp Ala Gly
 105 110 115

ctc ggt gga att gaa tgc ctc tcc gga atc ccc ggc tcc gcc ggc gcc 499
 Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro Gly Ser Ala Gly Ala
 120 125 130

acc cca gtc caa aac gtg ggc gcc tac ggc acg gaa gtt tcc gat gta 547
 Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr Glu Val Ser Asp Val
 135 140 145

ctc acc cgc gtc cag ctt ctc gac cgc acc acc cac caa gtc tcc tgg 595
 Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr His Gln Val Ser Trp
 150 155 160 165

gtc gac gcc tcc gaa ctc gac ctc tct tac cga tac tcc aat ctc aaa 643
 Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg Tyr Ser Asn Leu Lys
 170 175 180

ttc acc aac cgc gca gtc gtc ttg gcg atc gaa ctc cag ctc ctc acc 691
 Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu Leu Gln Leu Leu Thr
 185 190 195

gac gga ttg tcc gcg ccg cta cgt ttt ggt gaa ttg gga cgt cga tta 739
 Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu Leu Gly Arg Arg Leu
 200 205 210

gcg atc tcc gag gcc gaa ccc cac cca cgt cgc ccc gtc cgc atg gtc 787
 Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg Pro Val Arg Met Val
 215 220 225

cgc gac gcc gtc cta gaa ctc cgc cgc gcc aaa ggc atg gtc gtg gaa 835
 Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys Gly Met Val Val Glu
 230 235 240 245

cac acc gac cac gac acc tgg tcc gcc gga tcc ttc ttc acc aac cca 883
 His Thr Asp His Asp Thr Trp Ser Ala Gly Ser Phe Phe Thr Asn Pro
 250 255 260

atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa 931

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130 135 140
 Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr
 145 150 155 160
 His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg
 165 170 175
 Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu
 180 185 190
 Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu
 195 200 205
 Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg
 210 215 220
 Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys
 225 230 235 240
 Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser
 245 250 255
 Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe
 260 265 270
 Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly
 275 280 285
 Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys
 290 295 300
 Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His
 305 310 315 320
 Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val
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<212> DNA

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acc gct gtc acc gtg ttg acc atg cgt ctg gat gac ccc acc ggc tac 96

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Gly	Arg	Ile	Val	Arg	Asn	Glu	Glu	Gly	Glu	Val	Thr	Ala	Ile	Val	Glu		
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caa	aaa	gat	gct	tca	gca	gaa	gtc	caa	gcc	atc	gat	gag	gtc	aac	tcc	192	
Gln	Lys	Asp	Ala	Ser	Ala	Glu	Val	Gln	Ala	Ile	Asp	Glu	Val	Asn	Ser		
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Gly	Val	Phe	Ala	Phe	Asp	Ala	Ala	Ile	Leu	Arg	Ser	Ala	Leu	Ala	Glu		
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Leu	Lys	Ser	Asp	Asn	Ala	Gln	Gly	Glu	Leu	Tyr	Leu	Thr	Asp	Val	Leu		
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ggc	att	gct	cgt	ggc	gag	ggc	cac	cca	gtg	cgc	gcc	cac	acc	gcc	gcc	336	
Gly	Ile	Ala	Arg	Gly	Glu	Gly	His	Pro	Val	Arg	Ala	His	Thr	Ala	Ala		
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Asp	Ala	Arg	Glu	Leu	Ala	Gly	Val	Asn	Asp	Arg	Val	Gln	Leu	Ala	Glu		
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Glu	Thr	Val	Ile	Gly	Asp	Arg	Val	Glu	Val	Gly	Pro	Asp	Thr	Thr	Leu		
			180					185					190				
acc	aac	atg	acc	atc	ggc	gac	ggc	gca	tcc	gta	atc	cgc	acc	cac	ggt	624	
Thr	Asn	Met	Thr	Ile	Gly	Asp	Gly	Ala	Ser	Val	Ile	Arg	Thr	His	Gly		
		195					200					205					
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Phe	Asp	Ser	Thr	Ile	Gly	Glu	Asn	Ala	Thr	Val	Gly	Pro	Phe	Thr	Tyr		
	210					215					220						
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Val	Glu	Thr	Lys	Lys	Ala	Thr	Ile	Gly	Arg	Gly	Ser	Lys	Val	Pro	His		
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Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr
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Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala
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Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile
305                310                315

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Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln
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cga aac atc gaa ggc tgg gtg caa aag aag cgc cct gga acc gct gca 1056
Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala
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gca caa gcc gca gaa gcc gcc caa aac gtc cac aac cag gaa ggc 1101
Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly
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Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu
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Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala
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Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly
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acc ccg ggt att gaa ctt gtt gcc aaa gag gct gct gat ctt ggt gca 211
 Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala Ala Asp Leu Gly Ala
 25 30 35

act cgg tta gca att atc act gct ccg aac aaa gac gga att ctt aaa 259
 Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys Asp Gly Ile Leu Lys
 40 45 50

cac ttc gag gag ttc cct gag ctt gag gca act ctt gag gct cgc ggt 307
 His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr Leu Glu Ala Arg Gly
 55 60 65

aag act gat caa ctg aat aaa gtt cga gca gct cga gaa ttg att gca 355
 Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala Arg Glu Leu Ile Ala
 70 75 80 85

aca gtt cca gtg gtt caa gaa aag cca ttg ggg ctt ggt cac gct gtt 403
 Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly Leu Gly His Ala Val
 90 95 100

ggc ctt gct gag tct gtg ctc gat gat gat gaa gat gtt gtg gct gtc 451
 Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu Asp Val Val Ala Val
 105 110 115

atg ctg cca gac gat ttg gtg ctg cca ttt ggt gtg acc gag aga atg 499
 Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly Val Thr Glu Arg Met
 120 125 130

gca gaa gtt cgc gct aag ttt ggc gga tct gtt ctt gca gca att gag 547
 Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val Leu Ala Ala Ile Glu
 135 140 145

gtg gct gaa gat gaa gtc tca aat tac gga gta ttt aag ctc ggt gaa 595
 Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val Phe Lys Leu Gly Glu
 150 155 160 165

ctc gat gca gag tcc gaa agt gaa ggc att agg cgt gtt gta gga atg 643
 Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg Arg Val Val Gly Met
 170 175 180

gtt gaa aag cct gcg cct gaa gat gca cca tca agg ttt gcc gca acg 691
 Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Arg Phe Ala Ala Thr
 185 190 195

ggc cgt tat cta ctt gat cga gct att ttt gat gca ctg cgt cga att 739
 Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp Ala Leu Arg Arg Ile
 200 205 210

gag cct ggt gct ggt gga gaa ctg caa tta aca gat gcc atc gca tta 787
 Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr Asp Ala Ile Ala Leu
 215 220 225

ttg atc gaa gaa ggc cat ccg gta cac att gtg gtt cat gaa gga aag 835
 Leu Ile Glu Glu Gly His Pro Val His Ile Val Val His Glu Gly Lys
 230 235 240 245

cgc cat gac ctt ggt aat cca gct ggg tac att cct gct gtt gtg tac 883

002290" 0420960

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<212> PRT
<213> Corynebacterium glutamicum
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Leu	Pro	Val	Val 20	Asp	Thr	Pro	Gly	Ile 25	Glu	Leu	Val	Ala	Lys 30	Glu	Ala
Ala	Asp	Leu 35	Gly	Ala	Thr	Arg	Leu 40	Ala	Ile	Ile	Thr	Ala 45	Pro	Asn	Lys
Asp	Gly 50	Ile	Leu	Lys	His	Phe 55	Glu	Glu	Phe	Pro	Glu 60	Leu	Glu	Ala	Thr
Leu 65	Glu	Ala	Arg	Gly	Lys 70	Thr	Asp	Gln	Leu	Asn 75	Lys	Val	Arg	Ala	Ala 80
Arg	Glu	Leu	Ile	Ala 85	Thr	Val	Pro	Val	Val 90	Gln	Glu	Lys	Pro	Leu	Gly
Leu	Gly	His	Ala 100	Val	Gly	Leu	Ala	Glu 105	Ser	Val	Leu	Asp	Asp 110	Asp	Glu
Asp	Val	Val 115	Ala	Val	Met	Leu	Pro 120	Asp	Asp	Leu	Val	Leu 125	Pro	Phe	Gly
Val	Thr 130	Glu	Arg	Met	Ala	Glu 135	Val	Arg	Ala	Lys	Phe 140	Gly	Gly	Ser	Val
Leu 145	Ala	Ala	Ile	Glu	Val 150	Ala	Glu	Asp	Glu	Val 155	Ser	Asn	Tyr	Gly	Val 160
Phe	Lys	Leu	Gly	Glu 165	Leu	Asp	Ala	Glu	Ser 170	Glu	Ser	Glu	Gly	Ile 175	Arg
Arg	Val	Val	Gly 180	Met	Val	Glu	Lys	Pro 185	Ala	Pro	Glu	Asp	Ala 190	Pro	Ser
Arg	Phe	Ala 195	Ala	Thr	Gly	Arg	Tyr 200	Leu	Leu	Asp	Arg	Ala 205	Ile	Phe	Asp
Ala	Leu 210	Arg	Arg	Ile	Glu	Pro 215	Gly	Ala	Gly	Gly	Glu 220	Leu	Gln	Leu	Thr

[illegible]

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 Asp Val Val Ala Val Met Leu Pro His
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<210> 270
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 <213> Corynebacterium glutamicum

<400> 270

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		20						25					30		
Val	Pro	Lys	Glu	Leu	Leu	Pro	Val	Val	Asp	Thr	Pro	Gly	Ile	Glu	Leu
		35					40					45			
Ile	Ala	Ala	Glu	Ala	Ala	Glu	Leu	Gly	Ala	Thr	Arg	Leu	Ala	Ile	Ile
	50					55					60				
Thr	Ala	Pro	Asn	Lys	Ala	Gly	Val	Leu	Ala	His	Phe	Glu	Arg	Ser	Ser
65				70						75				80	
Glu	Leu	Glu	Glu	Thr	Leu	Met	Glu	Arg	Gly	Lys	Thr	Asp	Gln	Val	Glu
				85					90					95	
Ile	Ile	Arg	Arg	Ala	Ala	Asp	Leu	Ile	Lys	Ala	Val	Pro	Val	Thr	Gln
		100					105						110		
Asp	Lys	Pro	Leu	Gly	Leu	Gly	His	Ala	Val	Gly	Leu	Ala	Glu	Ser	Val
	115						120					125			
Leu	Asp	Asp	Asp	Glu	Asp	Val	Val	Ala	Val	Met	Leu	Pro	His		
	130					135					140				

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXA01262

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aaacttgctg tatcaataaa acacgaaaag gaatactttt atg aaa att gcc gtc 115
 Met Lys Ile Ala Val
 1 5

gca ggg ctc gga tat gtt ggg ctt tca aat gca gct ctc ctc tct aaa 163
 Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala Ala Leu Leu Ser Lys
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003290" 0420960

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ccccttaaag acaccctaaa cacgagtgaa ataggaacac atg act tta act gac 115
Met Thr Leu Thr Asp
1 5

aac agc aaa aac gtt gat gct gtc atc ttg gtc ggt ggc aaa ggt acc 163
Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val Gly Gly Lys Gly Thr
10 15 20

cga ctg cgc ccc ctg acc gtc aat act cca aag cca atg ctg cca act 211
Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys Pro Met Leu Pro Thr
25 30 35

gct ggc cac cca ttc ttg acc cac ctt ttg gcc cgc atc aag gcc gca 259
Ala Gly His Pro Phe Leu Thr His Leu Leu Ala Arg Ile Lys Ala Ala
40 45 50

ggc atc aca cac gtc gtg ctg gga acg tca ttc aaa gct gaa gtc ttc 307
Gly Ile Thr His Val Val Leu Gly Thr Ser Phe Lys Ala Glu Val Phe
55 60 65

gag gaa tac ttc gga gat ggc tcc gaa atg ggc ttg gaa att gaa tat 355
Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly Leu Glu Ile Glu Tyr
70 75 80 85

gtc gtc gag gat cag cct ttg ggc act ggt ggt ggc atc cga aac gtc 403
Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly Gly Ile Arg Asn Val
90 95 100

tac gac aag ctg cgt cac gat act gcg att gtg ttc aac ggc gat gtg 451
Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val Phe Asn Gly Asp Val
105 110 115

ctc tcc ggt gcg gat ctc aac agc att ctg gac acc cac cgc gaa aag 499
Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp Thr His Arg Glu Lys
120 125 130

gac gca gat ctg acc atg cat ctc gtg cgc gta gct aac cct cgt gcg 547
Asp Ala Asp Leu Thr Met His Leu Val Arg Val Ala Asn Pro Arg Ala
135 140 145

ttt ggt tgc gtc ccc acc gat gag gat ggt cgc gtc agc gaa ttc ctt 595
Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg Val Ser Glu Phe Leu
150 155 160 165

gaa aag acc gaa gat cca cca acc gat cag atc aac gcc ggc tgc tac 643
Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile Asn Ala Gly Cys Tyr
170 175 180

gtg ttc aag aag gaa ctc atc gag cag atc ccg gca ggc cga gca gtt 691
Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro Ala Gly Arg Ala Val
185 190 195

tcc gtc gag cgc gaa acc ttc cct cag ctg ttg gaa gaa ggc aag cga 739

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09602740.062290

Lys Ala Glu Val Phe Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly
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 Leu Glu Ile Glu Tyr Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly
 85 90 95
 Gly Ile Arg Asn Val Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val
 100 105 110
 Phe Asn Gly Asp Val Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp
 115 120 125
 Thr His Arg Glu Lys Asp Ala Asp Leu Thr Met His Leu Val Arg Val
 130 135 140
 Ala Asn Pro Arg Ala Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg
 145 150 155 160
 Val Ser Glu Phe Leu Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile
 165 170 175
 Asn Ala Gly Cys Tyr Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro
 180 185 190
 Ala Gly Arg Ala Val Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu
 195 200 205
 Glu Glu Gly Lys Arg Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg
 210 215 220
 Asp Met Gly Thr Pro Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val
 225 230 235 240
 Arg Gly Ile Ala Tyr Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser
 245 250 255
 Leu Val Asp Ala Ser Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly
 260 265 270
 Gly Thr Val Val Gly Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val
 275 280 285
 Asp Asn Thr Val Ile Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val
 290 295 300
 Ile Glu Asn Ser Ile Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala
 305 310 315 320
 His Ile Ser Gly Cys Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg
 325 330 335
 Cys Glu Leu Asn Ala Gly Met Arg Val Phe Pro Gly Val Val Ile Pro
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 Asp Ser Gly Ile Arg Phe Ser Ser Asp Gln
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<211> 1350

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 276

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Ala Gly Gly Glu Gly Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala
      20           25           30

Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val
      35           40           45

Leu Ser Asn Leu Val Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr
 50           55           60

Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn
 65           70           75           80

Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln
      85           90           95

Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln
      100          105          110

Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe
      115          120          125

Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu
      130          135          140

His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro
      145          150          155          160

Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly
      165          170          175

Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro
      180          185          190

Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr
      195          200          205

Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn
      210          215          220

Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg
      225          230          235          240

Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala
      245          250          255

Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala
      260          265          270

Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn
      275          280          285

Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu
      290          295          300

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00602740.062300

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Thr	Leu	Ile	Ala	Leu	Leu	Asp	Asn	Gly	Lys	Pro	Val	Ala	Gly	Val	Ile															
			105					110					115																	
tcc	gca	ccc	gca	ctg	gct	agg	cgt	tgg	tgg	gca	tcc	gaa	ggg	gcc	ggc	499														
Ser	Ala	Pro	Ala	Leu	Ala	Arg	Arg	Trp	Trp	Ala	Ser	Glu	Gly	Ala	Gly															
		120					125					130																		
gca	tgg	cgc	acc	ttc	aac	ggc	agc	tcc	cca	cgc	aaa	ctg	tcc	gtg	tcc	547														
Ala	Trp	Arg	Thr	Phe	Asn	Gly	Ser	Ser	Pro	Arg	Lys	Leu	Ser	Val	Ser															
	135					140					145																			
cag	gtg	tcc	aag	ctt	gac	gac	gcc	tcc	ctc	tcc	ttc	tcc	tcc	ctc	tcc	595														
Gln	Val	Ser	Lys	Leu	Asp	Asp	Ala	Ser	Leu	Ser	Phe	Ser	Ser	Leu	Ser															
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ggc	tgg	gcc	gaa	cga	gat	ttg	cgc	gat	cag	ttc	gtc	tcc	cta	act	gat	643														
Gly	Trp	Ala	Glu	Arg	Asp	Leu	Arg	Asp	Gln	Phe	Val	Ser	Leu	Thr	Asp															
				170					175					180																
acc	acc	tgg	cga	ctc	cgc	ggc	tac	ggc	gac	ttc	ttc	tcc	tac	tgc	ctc	691														
Thr	Thr	Trp	Arg	Leu	Arg	Gly	Tyr	Gly	Asp	Phe	Phe	Ser	Tyr	Cys	Leu															
			185					190					195																	
gtc	gcc	gaa	ggg	gcc	gtc	gat	atc	gcc	gct	gaa	cca	gaa	gtc	agc	ctc	739														
Val	Ala	Glu	Gly	Ala	Val	Asp	Ile	Ala	Ala	Glu	Pro	Glu	Val	Ser	Leu															
		200					205					210																		
tgg	gat	ctt	gct	ccc	ctg	tcc	atc	ctg	gtc	acc	gaa	gcc	gga	gga	aag	787														
Trp	Asp	Leu	Ala	Pro	Leu	Ser	Ile	Leu	Val	Thr	Glu	Ala	Gly	Gly	Lys															
	215					220					225																			
ttc	acc	tca	ctg	gct	ggc	gtc	gat	gga	cca	cac	ggg	ggc	gat	gca	gta	835														
Phe	Thr	Ser	Leu	Ala	Gly	Val	Asp	Gly	Pro	His	Gly	Gly	Asp	Ala	Val															
230					235					240					245															
gcc	acc	aac	ggc	atc	ctg	cac	gat	gag	acg	ctg	gat	cgt	tta	aaa		880														
Ala	Thr	Asn	Gly	Ile	Leu	His	Asp	Glu	Thr	Leu	Asp	Arg	Leu	Lys																
				250					255					260																
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<212> PRT

<213> Corynebacterium glutamicum

<400> 278

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Leu	Ala	Asp	Ser	Ile	Thr	Leu	Asp	Arg	Phe	Glu	Ala	Ser	Asp	Leu	Glu
		20						25					30		

Val	Ser	Ser	Lys	Pro	Asp	Met	Thr	Pro	Val	Ser	Asp	Ala	Asp	Leu	Ala
		35					40					45			

Thr	Glu	Glu	Ala	Leu	Arg	Glu	Lys	Ile	Ala	Thr	Ala	Arg	Pro	Ala	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

00602740 062300

gac gat tta gcc tta gcc ctc gaa ctc gcc gaa ctt gcc gat tcc atc 163
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile

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aac ttt gcc gtg gta gga cta tat ttc tac gac aat cgc gtg gtg gac 643
Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp Asn Arg Val Val Asp
170 175 180

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atc gcc aag tca atc aag cct tcc tcg cgt ggc gaa ctg gaa atc acc 691
 Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly Glu Leu Glu Ile Thr
 185 190 195

tcc gtt aac gat gcc tac ctc cag caa ggt gct tta act gtg cag cgc 739
 Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala Leu Thr Val Gln Arg
 200 205 210

ctg gac cgt ggc gat gtc tgg tta gat acc ggc aca atc gat tcc atg 787
 Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly Thr Ile Asp Ser Met
 215 220 225

tcc gag gcg tct tcc tat gtt gag gtc ctg caa aaa cgt acc ggc aac 835
 Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln Lys Arg Thr Gly Asn
 230 235 240 245

atc atc gga tcc ccc gaa gtc gct gcg tac cgc gaa ggt ttc atc aca 883
 Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg Glu Gly Phe Ile Thr
 250 255 260

gct gaa gaa ctc aca gtg ctt ggt gag gaa ctg aag aaa tca ggc tac 931
 Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu Lys Lys Ser Gly Tyr
 265 270 275

gga aac tac ctg ctg aga gct ttg taatttacgg tgtggttggtg gag 978
 Gly Asn Tyr Leu Leu Arg Ala Leu
 280 285

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<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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Ile Thr Lys Gly Ile Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro
 20 25 30

Met Val Tyr Tyr Pro Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp
 35 40 45

Ile Leu Ile Ile Thr Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu
 50 55 60

Leu Gly Asp Gly Ser Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln
 65 70 75 80

Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe
 85 90 95

Ile Gly Asp Asp Asp Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp
 100 105 110

Gly Ala Gln Leu Gly His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly
 115 120 125

Gly Ile Val Phe Ala Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val

0002290"0720960


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Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu
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Arg Glu Arg Thr Leu Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser
      35                      40                      45
Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr
      50                      55                      60
Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu
      65                      70                      75                      80
Gly Val Arg Val Arg Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser
      85                      90                      95
Val Trp Ala Gly Leu Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp
      100                     105                     110
Ala Ile Val Leu Ile His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly
      115                     120                     125
Met Ile Ala Arg Val Val Arg Lys Val His Glu Gly Ala Thr Ala Val
      130                     135                     140
Ile Pro Val Leu Pro Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp
      145                     150                     155                     160
Gly Gly Val Val Val Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val
      165                     170                     175
Gln Thr Pro Gln Gly Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu
      180                     185                     190
Lys Phe Phe Ala Asp Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala
      195                     200                     205
Ser Leu Met Glu Trp Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp
      210                     215                     220
Pro Met Ala Phe Lys Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln
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Arg Ile Thr Asp Glu Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp
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09602740 062900 002900


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Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys
10 15 20

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259
His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg
40 45 50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307
Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp
55 60 65

gtg	gtc	acg	gat	gcc	gat	cgt	gcg	gcc	gag	gcc	ttc	gtc	gca	ggc	gtt	355
Val	Val	Thr	Asp	Ala	Asp	Arg	Ala	Ala	Glu	Ala	Phe	Val	Ala	Gly	Val	
70					75					80					85	

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Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala
90 95 100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat 451
Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp
105 110 115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc 499
Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu
120 125 130

gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc 547
Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly
135 140 145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga 595
Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly
150 155 160 165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc 643
Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala
170 175 180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc 691

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 185 190 195

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 Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro
 200 205 210

gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc 787
 Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile
 215 220 225

gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg 835
 Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp
 230 235 240 245

gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gcg tgc 883
 Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys
 250 255 260

atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg 931
 Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala
 265 270 275

gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac 973
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<212> PRT

<213> Corynebacterium glutamicum

<400> 292

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 35 40 45

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50 55 60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65 70 75 80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
 85 90 95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
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09-06-2017 08:20

<213> Corynebacterium glutamicum

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[illegible]

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<213> Corynebacterium glutamicum

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35 40 45

Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
50 55 60

Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
65 70 75 80

Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
85 90 95

Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
100 105 110

Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
115 120 125

Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
130 135 140

Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
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<213> Corynebacterium glutamicum

<223> FRXA01332

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Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val

The figure consists of 12 diagrams, labeled 'a' through 'l', illustrating the construction of a 3D wireframe model of a human head and neck. The diagrams are arranged vertically. Diagram 'a' shows a simple rectangular box with dimensions. Diagram 'b' shows a more complex shape with additional dimensions. Diagram 'c' shows a head and neck model with various measurements. Diagram 'd' shows a head and neck model with a different set of measurements. Diagram 'e' shows a head and neck model with a different set of measurements. Diagram 'f' shows a head and neck model with a different set of measurements. Diagram 'g' shows a head and neck model with a different set of measurements. Diagram 'h' shows a head and neck model with a different set of measurements. Diagram 'i' shows a head and neck model with a different set of measurements. Diagram 'j' shows a head and neck model with a different set of measurements. Diagram 'k' shows a head and neck model with a different set of measurements. Diagram 'l' shows a head and neck model with a different set of measurements.

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Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp
50 55 60

SECRET

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				Met	Thr	Leu	Arg	Ile								
				1				5								
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Ala	Leu	Phe	Gly	Ala	Gly	Arg	Ile	Gly	His	Val	His	Ala	Ala	Asn	Ile	
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gct	gca	aac	cct	gat	ctt	gaa	ctc	gtt	gtt	atc	gcc	gat	cct	ttc	att	211
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Glu	Gly	Ala	Gln	Arg	Leu	Ala	Glu	Ala	Asn	Gly	Ala	Glu	Ala	Val	Ala	
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Ser	Pro	Asp	Glu	Val	Phe	Ala	Arg	Asp	Asp	Ile	Asp	Gly	Ile	Val	Ile	
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Gly	Ser	Pro	Thr	Ser	Thr	His	Val	Asp	Leu	Ile	Thr	Arg	Ala	Val	Glu	
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0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

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Thr	Gly 195	Ala	Asn	Val	Phe	Ser	Gln 200	Glu	Ile	Ala	Glu	Phe 205	Asn	Asp	Tyr
Asp 210	Gln	Val	Ile	Val	Thr	Leu 215	Arg	Gly	Ser	Lys	Gly 220	Glu	Leu	Ile	Asn
Ile 225	Val	Asn	Ser	Arg	His 230	Cys	Ser	Tyr	Gly	Tyr 235	Asp	Gln	Arg	Leu	Glu 240
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Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro Met Phe Cys Glu Lys																	100
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<211> 361

<212> PRT

<213> Corynebacterium glutamicum

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35 40 45

Glu Gln Val Gly Ala Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp
50 55 60

Lys Leu Ile Glu Asp Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr
65 70 75 80

Ala Gly His Val Asp Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro
85 90 95

Met Phe Cys Glu Lys Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn
100 105 110

Ile Ile Arg Glu Ile Asp Ala Ala Gly Ala Thr Val Gln Val Gly His
115 120 125

Gln Arg Arg Phe Asp Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp
130 135 140

Ala Gly Asp Leu Gly Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp
145 150 155 160

Ala Phe Pro Pro Pro Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe
165 170 175

Arg Asp Val Ser Leu His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly
180 185 190

Gln Asp Ile Val Glu Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro
195 200 205

Glu Ile Gly Ala Val Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr
210 215 220

Leu Ala Asp Gly Thr Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly
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Ile Val Gly Leu Asp Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly
260 265 270

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Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val
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Asn Ser Ile Arg Thr Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala
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Gln Gly Ile Ser Val Asn Ile
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 Met Ser Thr Ser Thr
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 Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys Ala Thr Ser Leu Ile
 10 15 20

cag ggt gtg gaa tat tac cga aat gcg gat cct tcc gaa act gtc ccg 211
 Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro Ser Glu Thr Val Pro
 25 30 35

ggt ttg atg cac gtc aaa ttc ggt gat tac cac gtt ggc gac att gaa 259
 Gly Leu Met His Val Lys Phe Gly Asp Tyr His Val Gly Asp Ile Glu
 40 45 50

ttc gtg gcc gcg ttc gac gtc gac gcc gaa aaa gta ggc atc gat ctt 307
 Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys Val Gly Ile Asp Leu
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 Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr Ile Lys Ile Ala Asp
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 Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly Pro Thr Leu Asp Gly
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 185 190 195

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 His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp
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 Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met
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ctt gac cgc aat cgc ttg gaa tcc aag aag gtc tcc aaa acc caa gca 835
 Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala
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gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac 883
 Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp
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cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac 931
 Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp
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 Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser
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 Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp
 310 315 320 325

cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag 1123
 Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys
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 145 150 155 160

Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu
 165 170 175

Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr
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 Leu Ala Ser Asp Leu
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 Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
 25 30 35

gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259
 Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
 40 45 50

gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct 307
 Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
 55 60 65

ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355
 Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
 70 75 80 85

00602740.062300

gat atc gtg aag qaa gtg ttg qaa gag gga ggc gtc gac aag cta aaa 307

Figure 1 consists of 12 sub-diagrams arranged in a 4x3 grid, illustrating the evolution of a rectangular hole in a domain. Each sub-diagram is labeled with a number from 1 to 12. The diagrams show a rectangular domain with a central hole. The hole's shape changes from a simple rectangle to a more complex, elongated shape, and finally to a highly irregular, fractal-like boundary. The diagrams are arranged in four rows and three columns. The first row shows the initial state (1, 2, 3). The second row shows the hole elongating (4, 5, 6). The third row shows the hole becoming more complex (7, 8, 9). The fourth row shows the hole becoming highly irregular (10, 11, 12). Each diagram includes a coordinate system with x and y axes. The diagrams are labeled with numbers 1 through 12. The diagrams show the evolution of a rectangular hole in a domain. The hole's shape changes from a simple rectangle to a more complex, elongated shape, and finally to a highly irregular, fractal-like boundary. The diagrams are arranged in four rows and three columns. The first row shows the initial state (1, 2, 3). The second row shows the hole elongating (4, 5, 6). The third row shows the hole becoming more complex (7, 8, 9). The fourth row shows the hole becoming highly irregular (10, 11, 12). Each diagram includes a coordinate system with x and y axes. The diagrams are labeled with numbers 1 through 12. The diagrams show the evolution of a rectangular hole in a domain. The hole's shape changes from a simple rectangle to a more complex, elongated shape, and finally to a highly irregular, fractal-like boundary. The diagrams are arranged in four rows and three columns. The first row shows the initial state (1, 2, 3). The second row shows the hole elongating (4, 5, 6). The third row shows the hole becoming more complex (7, 8, 9). The fourth row shows the hole becoming highly irregular (10, 11, 12). Each diagram includes a coordinate system with x and y axes. The diagrams are labeled with numbers 1 through 12.

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Tyr	Ala	Arg	Glu	Gly	Ala	Asp	Val	Ala	Ile	Ala	Tyr	Leu	Pro	Glu	Glu		
70					75				80						85		
caa	gcc	gat	gct	gac	aga	gtg	ctc	caa	gca	atc	gag	gaa	aca	ggt	caa	403	
Gln	Ala	Asp	Ala	Asp	Arg	Val	Leu	Gln	Ala	Ile	Glu	Glu	Thr	Gly	Gln		
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aaa	gct	ttt	tct	ttc	cct	ggt	gat	ctc	cgt	gat	cca	gaa	tac	tgt	cgc	451	
Lys	Ala	Phe	Ser	Phe	Pro	Gly	Asp	Leu	Arg	Asp	Pro	Glu	Tyr	Cys	Arg		
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tcg	ctg	gtc	caa	gag	acg	gtg	aac	gct	tta	ggt	ggc	cta	gac	atc	ttg	499	
Ser	Leu	Val	Gln	Glu	Thr	Val	Asn	Ala	Leu	Gly	Gly	Leu	Asp	Ile	Leu		
		120					125					130					
gtc	aac	aac	gcg	tca	cgt	cag	gtg	tgg	gca	cct	ggt	ttg	acc	gaa	att	547	
Val	Asn	Asn	Ala	Ser	Arg	Gln	Val	Trp	Ala	Pro	Gly	Leu	Thr	Glu	Ile		
	135					140					145						
acc	gac	gaa	aac	ttc	gac	cag	act	ttg	cag	gtt	aac	ctc	tat	ggt	agt	595	
Thr	Asp	Glu	Asn	Phe	Asp	Gln	Thr	Leu	Gln	Val	Asn	Leu	Tyr	Gly	Ser		
150					155				160						165		
ttt	cgg	gtt	acc	aaa	gca	gct	ata	cct	cat	ctg	aag	ccc	gga	tca	tcg	643	
Phe	Arg	Val	Thr	Lys	Ala	Ala	Ile	Pro	His	Leu	Lys	Pro	Gly	Ser	Ser		
				170					175					180			
ata	atc	ttt	aca	tcg	tcc	att	cag	gcg	tac	caa	cct	tcg	gaa	acc	ctc	691	
Ile	Ile	Phe	Thr	Ser	Ser	Ile	Gln	Ala	Tyr	Gln	Pro	Ser	Glu	Thr	Leu		
			185					190					195				
ttg	gat	tac	gcc	atg	act	aag	gcg	gca	ttg	aac	aat	ttg	tca	aag	ggc	739	
Leu	Asp	Tyr	Ala	Met	Thr	Lys	Ala	Ala	Leu	Asn	Asn	Leu	Ser	Lys	Gly		
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ttg	gca	agt	agt	ctg	ata	ggc	gat	ggc	att	cgg	gta	aat	tct	gta	gcc	787	
Leu	Ala	Ser	Ser	Leu	Ile	Gly	Asp	Gly	Ile	Arg	Val	Asn	Ser	Val	Ala		
	215					220					225						
cca	ggt	cct	ttc	tgg	acg	ccg	ttg	caa	ccc	agc	cat	ggt	cag	cca	caa	835	
Pro	Gly	Pro	Phe	Trp	Thr	Pro	Leu	Gln	Pro	Ser	His	Gly	Gln	Pro	Gln		
230					235					240					245		
gag	aaa	ata	gaa	gga	ttt	ggc	cag	cac	gct	ccg	att	gga	aga	gcg	ggt	883	
Glu	Lys	Ile	Glu	Gly	Phe	Gly	Gln	His	Ala	Pro	Ile	Gly	Arg	Ala	Gly		
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cac	cct	gtt	gag	ttg	gca	ggt	gcg	tac	gtt	ttt	ctc	gct	tct	gac	gaa	931	
His	Pro	Val	Glu	Leu	Ala	Gly	Ala	Tyr	Val	Phe	Leu	Ala	Ser	Asp	Glu		

003290"04220960

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 gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc 979
 Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro
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 acc cca tagtcggtac aagcgggaatc act 1008
 Thr Pro
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 <213> Corynebacterium glutamicum

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 35 40 45
 Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala
 50 55 60
 Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
 65 70 75 80
 Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
 85 90 95
 Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
 100 105 110
 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
 115 120 125
 Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
 130 135 140
 Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
 145 150 155 160
 Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
 165 170 175
 Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
 180 185 190
 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
 195 200 205
 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
 210 215 220
 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
 225 230 235 240

00E290"0420960

His	Gly	Gln	Pro	Gln	Glu	Lys	Ile	Glu	Gly	Phe	Gly	Gln	His	Ala	Pro
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Ile	Gly	Arg	Ala	Gly	His	Pro	Val	Glu	Leu	Ala	Gly	Ala	Tyr	Val	Phe
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Leu	Ala	Ser	Asp	Glu	Ala	Ser	Tyr	Val	Val	Gly	Glu	Thr	Leu	Gly	Val
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Thr	Gly	Gly	Thr	Pro	Thr	Pro									
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Met Ile Ser Leu Leu																5
aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc																163
Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser																20
cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att																211
Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile																35
ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct																259
Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala																50
ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct																307
Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala																65
tat gct cgc gag ggg gca gat gtt gcg atc gct tac ttg ccc gaa gaa																355
Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala Tyr Leu Pro Glu Glu																85
caa gcc gat gct gac aga gtg ctc caa gca atc gag gaa aca ggt caa																403
Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln																100
aaa gct ttt tct ttc cct ggt gat ctc cgt gat cca gaa tac tgt cgc																451
Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp Pro Glu Tyr Cys Arg																115
tcg ctg gtc caa gag acg gtg aac gct tta ggt ggc cta gac atc ttg																499
Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu																

120	125	130	
gtc aac aac gcg tca cgt cag gtg tgg gca cct ggt ttg acc gaa att			547
Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile			
135	140	145	
acc gac gaa aac ttc gac cag act ttg cag gtt aac ctc tat ggt agt			595
Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val Asn Leu Tyr Gly Ser			
150	155	160	165
ttt cgg gtt acc aaa gca gct ata cct cat ctg aag ccc gga tca tcg			643
Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu Lys Pro Gly Ser Ser			
	170	175	180
ata atc ttt aca tcg tcc att cag gcg tac caa cct tcg gaa acc ctc			691
Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln Pro Ser Glu Thr Leu			
	185	190	195
ttg gat tac gcc atg act aag gcg gca ttg aac aat ttg tca aag ggc			739
Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn Asn Leu Ser Lys Gly			
	200	205	210
ttg gca agt agt ctg ata ggc gat ggc att cgg gta aat tct gta gcc			787
Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg Val Asn Ser Val Ala			
	215	220	225
cca ggt cct ttc tgg acg ccg ttg caa ccc agc cat ggt cag cca caa			835
Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser His Gly Gln Pro Gln			
230	235	240	245
gag aaa ata gaa gga ttt ggc cag cac gct ccg att gga aga gcg ggt			883
Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro Ile Gly Arg Ala Gly			
	250	255	260
cac cct gtt gag ttg gca ggt gcg tac gtt ttt ctc gct tct gac gaa			931
His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe Leu Ala Ser Asp Glu			
	265	270	275
gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc			979
Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro			
	280	285	290
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Thr Pro			
295			

<210> 318

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

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			20					25					30		

Pro	Gln	Ala	Asp	Ile	Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu
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<400> 321
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 35 40 45
 Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
 50 55 60
 Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65 70 75 80
 Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
 85 90 95
 Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
 100 105 110
 Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
 115 120 125
 Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
 130 135 140
 Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
 145 150 155 160
 Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
 165 170 175
 Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
 180 185 190
 Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
 195 200 205
 Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
 210 215 220
 Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
 225 230 235 240
 Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
 245 250 255
 Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
 260 265 270
 Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
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 Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr
 290 295 300
 Val Lys Leu Asp Asn Val Ala Asp Phe Lys
 305 310

003330" 04220960

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<210> 327
<211> 1077
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXN00872
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ccacattcca tcaaaaatga gtgaagggtt gcatcgccac atg act aac ttg acg 115																
Met Thr Asn Leu Thr 5																
agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163																
Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr 20																
cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag 211																
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys 35																
tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat 259																
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His 50																
gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc 307																
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly 65																
gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac 355																
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr 85																
gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att 403																
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile 100																
ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct 451																
Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala 115																
ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc 499																
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg 130																
gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca 547																
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro 145																
agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc 595																
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg 165																
cac acc atc ttt gat ctg gac tac cga cca atg ttc tgg gaa tcc cca 643																
His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met Phe Trp Glu Ser Pro 180																

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Val	Asp	Asn	Gln	Tyr 85	Val	Ala	Thr	Asp	Gln 90	Thr	Phe	Lys	Thr	Pro 95	Val
Thr	Phe	Cys	Glu 100	Ile	Phe	Pro	Pro	Asp 105	Asp	Phe	Pro	Leu	Tyr 110	Phe	Tyr
Arg	Glu	Pro 115	Lys	Ala	Pro	Asp	Leu 120	Asn	Ile	Glu	Ser	Ala 125	Asp	Val	Ser
Leu	Asp 130	Asp	Val	Arg	Glu	Ala 135	Asp	Ile	Leu	Trp	Phe 140	Thr	Leu	Thr	Gly
Phe 145	Ser	Glu	Glu	Pro 150	Ser	Arg	Gly	Thr	His 155	Arg	Glu	Ile	Leu	Thr	Thr 160
Arg	Ala	Asn	Arg	Arg 165	His	Thr	Ile	Phe	Asp 170	Leu	Asp	Tyr	Arg	Pro 175	Met
Phe	Trp	Glu	Ser 180	Pro	Glu	Glu	Ala	Thr 185	Lys	Gln	Ala	Glu	Trp 190	Ala	Leu
Gln	His	Ser 195	Thr	Val	Ala	Val	Gly 200	Asn	Lys	Glu	Glu	Cys 205	Glu	Ile	Ala
Val	Gly 210	Glu	Thr	Glu	Pro	Glu 215	Arg	Ala	Gly	Arg	Ala 220	Leu	Leu	Glu	Arg
Gly 225	Val	Glu	Leu	Ala	Ile 230	Val	Lys	Gln	Gly	Pro 235	Lys	Gly	Val	Met	Ala 240
Met	Thr	Lys	Asp	Glu 245	Thr	Val	Glu	Val	Pro 250	Pro	Phe	Phe	Val	Asp 255	Val
Ile	Asn	Gly	Leu 260	Gly	Ala	Gly	Asp	Ala 265	Phe	Gly	Gly	Ala	Leu 270	Cys	His
Gly	Leu	Leu 275	Ser	Glu	Trp	Pro	Leu 280	Glu	Lys	Val	Leu	Arg 285	Phe	Ala	Asn
Thr	Ala 290	Gly	Ala	Leu	Val	Ala 295	Ser	Arg	Leu	Glu	Cys 300	Ser	Thr	Ala	Met
Pro 305	Thr	Thr	Asp	Glu	Val 310	Glu	Ala	Ser	Leu	Asn 315	Gln	Lys	Val		

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<213> Corynebacterium glutamicum
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Met Thr Asn Leu Thr

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Ser	Thr	His	Glu	Val	Leu	Ala	Ile	Gly	Arg	Leu	Gly	Val	Asp	Ile	Tyr			
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cca	ctt	caa	agt	gga	gta	gga	ctg	gcc	gat	gtt	caa	tct	ttc	ggc	aag	211		
Pro	Leu	Gln	Ser	Gly	Val	Gly	Leu	Ala	Asp	Val	Gln	Ser	Phe	Gly	Lys			
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tac	ctc	ggc	gga	agc	gca	gca	aac	gtt	tct	gtt	gca	gcc	gcc	cgc	cat	259		
Tyr	Leu	Gly	Gly	Ser	Ala	Ala	Asn	Val	Ser	Val	Ala	Ala	Ala	Arg	His			
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gga	cac	aat	tcc	gca	ctg	ctg	tcc	cgt	gtg	gga	aat	gat	cct	ttc	ggc	307		
Gly	His	Asn	Ser	Ala	Leu	Leu	Ser	Arg	Val	Gly	Asn	Asp	Pro	Phe	Gly			
				55						60						65		
gag	tac	ctg	ctt	gct	gag	ctg	gag	cgt	ttg	ggc	gtg	gac	aac	cag	tac	355		
Glu	Tyr	Leu	Leu	Ala	Glu	Leu	Glu	Arg	Leu	Gly	Val	Asp	Asn	Gln	Tyr			
				70						75						80		
gtt	gcc	acc	gat	cag	act	ttt	aag	acc	cca	gtg	acc	ttc	tgt	gaa	att	403		
Val	Ala	Thr	Asp	Gln	Thr	Phe	Lys	Thr	Pro	Val	Thr	Phe	Cys	Glu	Ile			
				90						95						100		
ttc	cca	ccg	gat	gat	ttc	cca	ctg	tac	ttc	tac	cgc	gaa	cca	aag	gct	451		
Phe	Pro	Pro	Asp	Asp	Phe	Pro	Leu	Tyr	Phe	Tyr	Arg	Glu	Pro	Lys	Ala			
				105						110						115		
ccg	gat	ctc	aat	att	gaa	tcc	gca	gac	gtc	agc	ctg	gac	gat	gtg	cgc	499		
Pro	Asp	Leu	Asn	Ile	Glu	Ser	Ala	Asp	Val	Ser	Leu	Asp	Asp	Val	Arg			
				120						125						130		
gaa	gcc	gat	att	ttg	tgg	ttc	aca	ctc	act	ggc	ttc	agt	gaa	gag	cca	547		
Glu	Ala	Asp	Ile	Leu	Trp	Phe	Thr	Leu	Thr	Gly	Phe	Ser	Glu	Glu	Pro			
				135						140						145		
agc	cgc	ggc	aca	cac	cgc	gag	atc	ttg	act	act	cgt	gcg	aac	cgt	cgc	595		
Ser	Arg	Gly	Thr	His	Arg	Glu	Ile	Leu	Thr	Thr	Arg	Ala	Asn	Arg	Arg			
				150						155						160		
cac	acc	atc	ttt	gat	ctg	gac	tac	cga										622
His	Thr	Ile	Phe	Asp	Leu	Asp	Tyr	Arg										
				170														

<210> 330

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

$\langle 400 \rangle$ 330

Met Thr Asn Leu Thr Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu
1 5 10 15

Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val
20 25 30

Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val
35 40 45

[illegible]

70	75	80	85	
tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac ccg				403
Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn Pro	90	95	100	
atc acg ggt gtt cct ttc acc gag cct gtg ctg gca act tct tcc act				451
Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser Thr	105	110	115	
gaa aat gcc att aac ctg cgc aat cag cgt tac tta att gtt cgt gac				499
Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg Asp	120	125	130	
aac ctg cca gct cgt ggg ctt gct act tgg acc aat gct gtt cag gaa				547
Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln Glu	135	140	145	
gtc gcg gag cga tcc cgt ttg ggt att cct gtt gcg ttt gcg tcg aat				595
Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser Asn	150	155	160	165
cct cgt aac cac gtc gcg ctc gtt gcg cag ttc ggt gtg aac gag tcc				643
Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu Ser	170	175	180	
gcg ggt gtg ttc tct gag tgg cct ggc gag ctg ggt ctt gct gcg ctt				691
Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala Leu	185	190	195	
cgc gat gct gaa ctg atg gag act ttc ggt acc gag gct gct aaa gaa				739
Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys Glu	200	205	210	
tgg cgt gcc ggt ggt gtg cac aag ctg tac ggt tac atg gct gac ctc				787
Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp Leu	215	220	225	
gct tct gag cct cgt tgg tcc cgc ttc aac ggt act ttt ggt gag gat				835
Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu Asp	230	235	240	245
ccg gag ttg atc tct gat tac atc gct gct gtt gtg cgt ggt ttg cag				883
Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu Gln	250	255	260	
ggc cct gag ctg tcc aag aat tcc gtg tcg acc acc att aag cac ttc				931
Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His Phe	265	270	275	
cca ggt ggc ggc gtg cgc ctc gac ggc cac gat cct cac ttc cac tgg				979
Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp Pro His Phe His Trp	280	285	290	
ggt cag acc aat gag tac cca acc gaa gat gcg ctg ggc aag tac cat				1027
Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala Leu Gly Lys Tyr His	295	300	305	
ctg cct cct ttc cag gca gct atc gac gct ggc tgc gcc tcg atc atg				1075
Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly Cys Ala Ser Ile Met	310	315	320	325

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cct tac tac gca cgg cca atg aac aac tcc gcc aac cag ctc gat cag 1123
 Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala Asn Gln Leu Asp Gln
 330 335 340

cag ctg tgg caa aac ccg acc acg cag ttc gaa gag gtt gcg ttt gcc 1171
 Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu Glu Val Ala Phe Ala
 345 350 355

tac aac cgc acc ttc att cag gat ttg ctt cgc gac gcc atg ggc cac 1219
 Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly His
 360 365 370

cgt ggg tac gtc aac tcc gac tcc ggc gtc atc gac gcc atg atg tgg 1267
 Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met Trp
 375 380 385

ggc gtg gag gaa ctc agc gag cca gaa cgc ttc gcc gca gca gtg cgt 1315
 Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe Ala Ala Ala Val Arg
 390 395 400 405

gca ggc acc gac att ttc tcc gac atg gct aac cca cgt cga ctg ctc 1363
 Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn Pro Arg Arg Leu Leu
 410 415 420

gaa gca gtt gct gag gga cac ctt gat gag tca gag ctg aat cag cca 1411
 Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser Glu Leu Asn Gln Pro
 425 430 435

gtc cag cga ctc ctg gag gaa atc ttc cag ctt ggt ctg ttt gag aac 1459
 Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu Gly Leu Phe Glu Asn
 440 445 450

cca tat gtc tct gaa gat gaa gca gaa aag atc att ggt gcg cca gag 1507
 Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro Glu
 455 460 465

gtt tct gca ttg ggc aac aaa gca cag ctt gat tcc gtc acc ttg ctg 1555
 Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Leu Leu
 470 475 480 485

cgt aac aac ccc atc cgt gct gcc act gga tcc tgc agc aag cct gaa 1603
 Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro Glu
 490 495 500

gat cta ccc att ggt tac tgg ccg tac caa gat cga cga ggt tca act 1651
 Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser Thr
 505 510 515

aca gct gga agc agc cat tcg cgc aga act ccc agg ggt aac ctt ggt 1699
 Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro Arg Gly Asn Leu Gly
 520 525 530

gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc 1744
 Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg Val Gly Ser Pro
 535 540 545

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<210> 332

006290" 04230960

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

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Glu Gln Asp Gly Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu
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Ala Pro Tyr Glu Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp
35 40 45

Leu Val Lys Arg Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile
50 55 60

Gly Ser His Tyr Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly
65 70 75 80

Lys Asp Ala Glu Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp
85 90 95

Arg Glu Asp Asn Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu
100 105 110

Ala Thr Ser Ser Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr
115 120 125

Leu Ile Val Arg Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr
130 135 140

Asn Ala Val Gln Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val
145 150 155 160

Ala Phe Ala Ser Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe
165 170 175

Gly Val Asn Glu Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu
180 185 190

Gly Leu Ala Ala Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr
195 200 205

Glu Ala Ala Lys Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly
210 215 220

Tyr Met Ala Asp Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly
225 230 235 240

Thr Phe Gly Glu Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val
245 250 255

Val Arg Gly Leu Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr
260 265 270

Thr Ile Lys His Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp
275 280 285

Pro His Phe His Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala
290 295 300

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[illegible]

Gln	Gly	Pro	Glu	Leu	Ser	Lys	Asn	Ser	Val	Ser	Thr	Thr	Ile	Lys	His	
				245					250					255		
ttc	cca	ggg	ggc	ggc	gtg	cgc	ctc	gac	ggc	cac	gat	cct	cac	ttc	cac	816
Phe	Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His	
			260					265					270			
tgg	ggg	cag	acc	aat	gag	tac	cca	acc	gaa	gat	gcg	ctg	ggc	aag	tac	864
Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr	
		275					280					285				
cat	ctg	cct	cct	ttc	cag	gca	gct	atc	gac	gct	ggc	tgc	gcc	tcg	atc	912
His	Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile	
	290					295					300					
atg	cct	tac	tac	gca	cgg	cca	atg	aac	aac	tcc	gcc	aac	cag	ctc	gat	960
Met	Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp	
305					310					315					320	
cag	cag	ctg	tgg	caa	aac	ccg	acc	acg	cag	ttc	gaa	gag	gtt	gcg	ttt	1008
Gln	Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe	
				325					330					335		
gcc	tac	aac	cgc	acc	ttc	att	cag	gat	ttg	ctt	cgc	gac	gcc	atg	ggc	1056
Ala	Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly	
			340					345					350			
cac	cgt	ggg	tac	gtc	aac	tcc	gac	tcc	ggc	gtc	atc	gac	gcc	atg	atg	1104
His	Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met	
		355					360					365				
tgg	ggc	gtg	gag	gaa	ctc	agc	gag	cca	gaa	cgc	ttc	gcc	gca	gca	gtg	1152
Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val	
	370					375					380					
cgt	gca	ggc	acc	gac	att	ttc	tcc	gac	atg	gct	aac	cca	cgt	cga	ctg	1200
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu	
385					390					395					400	
ctc	gaa	gca	gtt	gct	gag	gga	cac	ctt	gat	gag	tca	gag	ctg	aat	cag	1248
Leu	Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln	
				405					410					415		
cca	gtc	cag	cga	ctc	ctg	gag	gaa	atc	ttc	cag	ctt	ggg	ctg	ttt	gag	1296
Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu	
			420					425					430			
aac	cca	tat	gtc	tct	gaa	gat	gaa	gca	gaa	aag	atc	att	ggg	gcg	cca	1344
Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro	
		435					440					445				
gag	gtt	tct	gca	ttg	ggc	aac	aaa	gca	cag	ctt	gat	tcc	gtc	acc	ttg	1392
Glu	Val	Ser	Ala	Leu	Gly	Asn	Lys	Ala	Gln	Leu	Asp	Ser	Val	Thr	Leu	
	450					455					460					
ctg	cgt	aac	aac	ccc	atc	cgt	gct	gcc	act	gga	tcc	tgc	agc	aag	cct	1440
Leu	Arg	Asn	Asn	Pro	Ile	Arg	Ala	Ala	Thr	Gly	Ser	Cys	Ser	Lys	Pro	
465					470					475					480	
gaa	gat	cta	ccc	att	ggg	tac	tgg	ccg	tac	caa	gat	cga	cga	ggg	tca	1488
Glu	Asp	Leu	Pro	Ile	Gly	Tyr	Trp	Pro	Tyr	Gln	Asp	Arg	Arg	Gly	Ser	

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<210> 334
<211> 528
<212> PRT
<213> Corynebacterium glutamicum
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Asp	Trp	Arg	Leu 20	Thr	Pro	Ala	Glu	Arg 25	Ala	Ala	Asp	Leu	Val 30	Lys	Arg
Met	Asn	Val 35	Glu	Glu	Lys	Ala	Gly 40	Leu	Met	Ile	Ile	Gly 45	Ser	His	Tyr
Pro	Gly 50	Tyr	Ser	Pro	Leu	Ala 55	Pro	Glu	Ser	Glu	Gly 60	Lys	Asp	Ala	Glu
Lys 65	Cys	Glu	Pro	Leu	Leu 70	Asn	Pro	Val	Asp	Met 75	Trp	Arg	Glu	Asp	Asn 80
Pro	Ile	Thr	Gly	Val 85	Pro	Phe	Thr	Glu	Pro 90	Val	Leu	Ala	Thr	Ser 95	Ser
Thr	Glu	Asn	Ala 100	Ile	Asn	Leu	Arg	Asn 105	Gln	Arg	Tyr	Leu	Ile 110	Val	Arg
Asp	Asn	Leu 115	Pro	Ala	Arg	Gly	Leu 120	Ala	Thr	Trp	Thr	Asn 125	Ala	Val	Gln
Glu	Val 130	Ala	Glu	Arg	Ser	Arg 135	Leu	Gly	Ile	Pro	Val 140	Ala	Phe	Ala	Ser
Asn 145	Pro	Arg	Asn	His	Val 150	Ala	Leu	Val	Ala	Gln 155	Phe	Gly	Val	Asn	Glu 160
Ser	Ala	Gly	Val 165	Phe	Ser	Glu	Trp	Pro	Gly 170	Glu	Leu	Gly	Leu 175	Ala	Ala
Leu	Arg	Asp	Ala 180	Glu	Leu	Met	Glu	Thr 185	Phe	Gly	Thr	Glu	Ala 190	Ala	Lys
Glu	Trp	Arg 195	Ala	Gly	Gly	Val	His 200	Lys	Leu	Tyr	Gly	Tyr 205	Met	Ala	Asp
Leu 210	Ala	Ser	Glu	Pro	Arg	Trp 215	Ser	Arg	Phe	Asn	Gly 220	Thr	Phe	Gly	Glu

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[illegible]

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 <211> 1632
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1609)
 <223> RXA00032

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 Met Asn Thr Pro Leu
 1 5
 cag ctc aac act gaa aac ctg cag gaa atc gct tcg act tcc gga gtg 163
 Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala Ser Thr Ser Gly Val
 10 15 20
 cag atc cca gcg ttc aac cgc gct gac gtc gcc ccg ggc att gtc cac 211
 Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala Pro Gly Ile Val His
 25 30 35
 ttc ggt gtt ggc gga ttc cat cgc gct cac caa gcg atg tac ctc aat 259
 Phe Gly Val Gly Gly Phe His Arg Ala His Gln Ala Met Tyr Leu Asn
 40 45 50
 gaa ttg atg aat gag ggc aag gcc ttg gat tgg ggc atc atc ggc atg 307
 Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp Gly Ile Ile Gly Met
 55 60 65
 ggt gtc atg cct tcc gat gtg cgc atg cgc gat gcc ctg gcc agc caa 355
 Gly Val Met Pro Ser Asp Val Arg Met Arg Asp Ala Leu Ala Ser Gln
 70 75 80 85
 gat cac ctt tat acc ctg acc act aaa gct cct gat gga act ctt gat 403
 Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro Asp Gly Thr Leu Asp
 90 95 100
 caa aaa atc atc gga tcc atc att gac tac gtg ttc gct ccc gag gac 451
 Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val Phe Ala Pro Glu Asp
 105 110 115
 cca gca cgg gcc gtt gca acc ctc gcg cag gac tcc atc cgc att gtt 499
 Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp Ser Ile Arg Ile Val
 120 125 130
 tcc ctc acg gtg act gaa ggc gga tac aac atc gat ccg gcg aca gaa 547
 Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile Asp Pro Ala Thr Glu
 135 140 145
 gat ttc gac cac acc aac cct cga atc gtt gct gac cgc gaa gcc ctg 595
 Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala Asp Arg Glu Ala Leu
 150 155 160 165
 cag gcg ggc gat act tcc act ttg cag acc ttc ttt ggg ttg atc act 643
 Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe Phe Gly Leu Ile Thr
 170 175 180

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0960270-0

Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn Pro Ile Lys Ile Val
 425 430 435

gac cgt ttg agt gag cgc gtc caa gaa aac gca tca gga aat cgc acc 1459
 Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala Ser Gly Asn Arg Thr
 440 445 450

gat att ttg tca ttc atc cgc gac cgt gga atc ttc gga gac ttg gtc 1507
 Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile Phe Gly Asp Leu Val
 455 460 465

gat gct gaa cca ttc acc aag gca tac tcc gag aca ctg tcc tcc ctt 1555
 Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu Thr Leu Ser Ser Leu
 470 475 480 485

cat gac cgt ggc gcg gaa gca acc atc gat gca ctt ctt acg cag gta 1603
 His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala Leu Leu Thr Gln Val
 490 495 500

act gtc taaatccggt gcgcgctagg gtt 1632
 Thr Val

<210> 336

<211> 503

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

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 20 25 30

Pro Gly Ile Val His Phe Gly Val Gly Gly Phe His Arg Ala His Gln
 35 40 45

Ala Met Tyr Leu Asn Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp
 50 55 60

Gly Ile Ile Gly Met Gly Val Met Pro Ser Asp Val Arg Met Arg Asp
 65 70 75 80

Ala Leu Ala Ser Gln Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro
 85 90 95

Asp Gly Thr Leu Asp Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val
 100 105 110

Phe Ala Pro Glu Asp Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp
 115 120 125

Ser Ile Arg Ile Val Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile
 130 135 140

Asp Pro Ala Thr Glu Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala
 145 150 155 160

Asp Arg Glu Ala Leu Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe

006290" 04220960

Val Gly Val Ile Val Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser
 65 70 75 80
 Leu Gln Thr Ile Gln Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu
 85 90 95
 Val Ala Glu Ala Asn Ser Val Gln Ala Gln Asp Val Val Met Glu Ser
 100 105 110
 Leu Ile Ser Ile Gln Ala Ala Gly Ile Ile His Val Pro Val Val Gly
 115 120 125
 Ser Ile Ala Pro Glu Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu
 130 135 140
 Leu Gly Pro Gly Phe Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe
 145 150 155 160
 Phe Gln Leu Thr Glu Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala
 165 170 175
 Ala Leu Val Gly Glu Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg
 180 185 190
 Gly Ile Ser His Ala Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His
 195 200 205
 Phe Gly His Tyr Ser Val Glu Ser Gly Glu Glu Met Ala Gln Val Val
 210 215 220
 Phe Asn Asn Gly Leu Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu
 225 230 235 240
 Met Ala Gly Val Met Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro
 245 250 255
 His Asp Val Val Ile Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe
 260 265 270
 Val Gly Ala Gly Ile Thr Thr Phe Val Pro Pro His Glu Glu Met Gly
 275 280 285
 Lys Glu Ala Val Arg Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu
 290 295 300
 Pro Thr Gly Asp Val Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser
 305 310 315 320
 Ser Thr His Ser Gly
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<210> 339

<211> 1246

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<400> 339

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                                         Met Gly Gln Cys Thr
                                         1 5
gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga 163
Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg
          10          15          20
gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc 211
Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile
          25          30          35
cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt 259
His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val
          40          45          50
ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa 307
Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu
          55          60          65
gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca 355
Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr
          70          75          80          85
att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag 403
Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln
          90          95          100
gtg atg gga aca aag ggt gcc acc atg acg atc ctg gaa ttc cct gaa 451
Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile Leu Glu Phe Pro Glu
          105          110          115
ggt acc gac ggc agg ctc att gtt cgc agt gaa aac gac acc cgt cga 499
Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu Asn Asp Thr Arg Arg
          120          125          130
aac cac ccc att cca ccc cgc gga tct tta tcc caa tgc cga tct ttc 547
Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser Gln Cys Arg Ser Phe
          135          140          145
cat cat caa cgg tgc ttt gat ccc gta tca cac cgc cca gat cgc aga 595
His His Gln Arg Cys Phe Asp Pro Val Ser His Arg Pro Asp Arg Arg
          150          155          160          165
ctt tat cga tgc gct caa cga agg ccg ccc acc act gat cac cgg ccg 643
Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr Thr Asp His Arg Pro
          170          175          180
cga tgc cac cag agc tct gaa agt tct cct tgg tgt cta cga atc agc 691
Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp Cys Leu Arg Ile Ser
          185          190          195
agc cac cca cca gcc ggt ctc ttt gat cta acg gaa gct ttt aaa acg 739
Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr Glu Ala Phe Lys Thr
          200          205          210

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 Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser Leu Ser Thr Pro Pro
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 gat caa cta gtg cgc ctc gca gct gcc act ggt ttc tcc ttt gtc ggt 835
 Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly Phe Ser Phe Val Gly
 230 235 240 245
 ctg cgc gtc atc gca gta acc ccc aac gaa cgt gta tat gac ctt tcc 883
 Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg Val Tyr Asp Leu Ser
 250 255 260
 cca gga tcc cca ctg ctg gct gca acc caa caa gcg ttg aaa gaa acc 931
 Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln Ala Leu Lys Glu Thr
 265 270 275
 gcc ctg tat gtg ctc gac act gaa ttc cta cag gta aac gca gac acc 979
 Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln Val Asn Ala Asp Thr
 280 285 290
 acc cgc gag gcc tgg ctt ccc gca cta gaa gcc gcc gga gca ctg gga 1027
 Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala Ala Gly Ala Leu Gly
 295 300 305
 gct aaa acc ttc acc atc gcc gcc ggt gat gac aac att gcg ccc ctg 1075
 Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp Asn Ile Ala Pro Leu
 310 315 320 325
 acc gac acg atc ggt gcc atg gtt gac gat gcc cgt gat ttc gga gtc 1123
 Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala Arg Asp Phe Gly Val
 330 335 340
 acc cca gcc cta gag cca atc tct tac cgc agc gtg cat tcc att ccg 1171
 Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser Val His Ser Ile Pro
 345 350 355
 cag gca gca gca atc gcc aga gac tcc ggc gga aaa gtc gtg gcg gac 1219
 Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly Lys Val Val Ala Asp
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 acc ttg cac atg gcc agg ttc gga gcc 1246
 Thr Leu His Met Ala Arg Phe Gly Ala
 375 380

<210> 340

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr
 1 5 10 15
 Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
 20 25 30
 Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly
 35 40 45
 Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp

0032290" 04220960

50		55		60												
Asn 65	Ile	Glu	Val	Glu	Asp	Ser	Ala	Val	Ala	Thr	Val	Arg	Phe	Glu	Ser	80
Gly	Ala	Leu	Ala	Thr	Ile	Ser	Ala	Thr	Thr	Ala	Ala	Glu	Pro	Ala	Leu	95
Gly	Ala	Gln	Val	Gln	Val	Met	Gly	Thr	Lys	Gly	Ala	Thr	Met	Thr	Ile	110
Leu	Glu	Phe	Pro	Glu	Gly	Thr	Asp	Gly	Arg	Leu	Ile	Val	Arg	Ser	Glu	125
Asn	Asp	Thr	Arg	Arg	Asn	His	Pro	Ile	Pro	Pro	Arg	Gly	Ser	Leu	Ser	140
Gln	Cys	Arg	Ser	Phe	His	His	Gln	Arg	Cys	Phe	Asp	Pro	Val	Ser	His	160
Arg	Pro	Asp	Arg	Arg	Leu	Tyr	Arg	Cys	Ala	Gln	Arg	Arg	Pro	Pro	Thr	175
Thr	Asp	His	Arg	Pro	Arg	Cys	His	Gln	Ser	Ser	Glu	Ser	Ser	Pro	Trp	190
Cys	Leu	Arg	Ile	Ser	Ser	His	Pro	Pro	Ala	Gly	Leu	Phe	Asp	Leu	Thr	205
Glu	Ala	Phe	Lys	Thr	Ser	Arg	Gln	Ile	Gly	Leu	Ala	Pro	Leu	Ser	Ser	220
Leu	Ser	Thr	Pro	Pro	Asp	Gln	Leu	Val	Arg	Leu	Ala	Ala	Ala	Thr	Gly	240
Phe	Ser	Phe	Val	Gly	Leu	Arg	Val	Ile	Ala	Val	Thr	Pro	Asn	Glu	Arg	255
Val	Tyr	Asp	Leu	Ser	Pro	Gly	Ser	Pro	Leu	Leu	Ala	Ala	Thr	Gln	Gln	270
Ala	Leu	Lys	Glu	Thr	Ala	Leu	Tyr	Val	Leu	Asp	Thr	Glu	Phe	Leu	Gln	285
Val	Asn	Ala	Asp	Thr	Thr	Arg	Glu	Ala	Trp	Leu	Pro	Ala	Leu	Glu	Ala	300
Ala	Gly	Ala	Leu	Gly	Ala	Lys	Thr	Phe	Thr	Ile	Ala	Ala	Gly	Asp	Asp	320
Asn	Ile	Ala	Pro	Leu	Thr	Asp	Thr	Ile	Gly	Ala	Met	Val	Asp	Asp	Ala	335
Arg	Asp	Phe	Gly	Val	Thr	Pro	Ala	Leu	Glu	Pro	Ile	Ser	Tyr	Arg	Ser	350
Val	His	Ser	Ile	Pro	Gln	Ala	Ala	Ala	Ile	Ala	Arg	Asp	Ser	Gly	Gly	365
Lys	Val	Val	Ala	Asp	Thr	Leu	His	Met	Ala	Arg	Phe	Gly	Ala			380

003290"0420960


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<211> 412
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(412)  
<223> FRXA00309
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gcttctggcc cgcggctcaa aaaatgaaaa aggagccgtc atg ggc caa tgc acg															115
Met Gly Gln Cys Thr															
1 5															
gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga															163
Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg															
10 15 20															
gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc															211
Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile															
25 30 35															
cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt															259
His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val															
40 45 50															
ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa															307
Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu															
55 60 65															
gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca															355
Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr															
70 75 80 85															
att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag															403
Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln															
90 95 100															
gtg atg gga															412
Val Met Gly															

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<210> 342
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<212> PRT
<213> Corynebacterium glutamicum
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Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
20 25 30
Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly

[illegible]

35 40 45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
50 55 60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
65 70 75 80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
85 90 95

Gly Ala Gln Val Gln Val Met Gly
100

<210> 343
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> RXN00310

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aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115
Met Ser Asp Lys Ile
1 5
tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163
Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
10 15 20
gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211
Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
25 30 35
gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259
Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
40 45 50
ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307
Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
55 60 65
gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
70 75 80 85
gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403
Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
90 95 100
gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451
Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
105 110 115
gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499

002290" 0420950


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<212> PRT
<213> Corynebacterium glutamicum
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<400> 346

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			20					25					30		
Ser	Ala	Val	Cys	Asp	Val	Asp	Gly	Ala	Lys	Ala	Ser	Glu	Thr	Ala	Ala
		35					40					45			
Lys	Tyr	Gly	Ile	Ser	Pro	Ser	Phe	Thr	Ser	Val	Asp	Glu	Ile	Leu	Ala
	50					55					60				
Ser	Gly	Val	Asp	Ile	Val	Ala	Val	Cys	Thr	Pro	His	Pro	Thr	His	Glu

65	70	75	80
Thr Val Val Leu Ala Ala Ala Ala Ala Gly Val His Val Leu Cys Glu	85	90	95
Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala	100	105	110
Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe	115	120	125
Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala	130	135	140
Arg			
145			

<210> 347
 <211> 1342
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1342)
 <223> RXA00041

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 Met His Thr Glu Leu
 1 5
 tcc agt ttg cgc cct gcg tac cat gtg act cct ccg cag ggc agg ctc 163
 Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro Pro Gln Gly Arg Leu
 10 15 20
 aat gat ccc aac gga atg tac gtc gat ggc gat acc ctc cac gtc tac 211
 Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp Thr Leu His Val Tyr
 25 30 35
 tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggc tgg 259
 Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly Trp
 40 45 50
 gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg acg 307
 Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp Thr
 55 60 65
 cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat gga 355
 His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp Gly
 70 75 80 85
 tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt ttc 403
 Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu Phe
 90 95 100
 tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa aac 451
 Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln Asn

00602740.062300

105				110				115								
ctc	gtc	gaa	gtc	gag	gac	cca	act	ggg	ctg	atg	ggc	ggc	att	cat	cgc	499
Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His	Arg	
		120					125					130				
cgt	tcg	cct	aaa	aat	ccg	ctt	atc	gac	gga	ccc	gcc	agc	ggg	ttc	aca	547
Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe	Thr	
	135					140					145					
ccc	cat	tac	cgc	gat	ccc	atg	atc	agc	cct	gat	ggg	gat	ggg	tgg	aaa	595
Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp	Lys	
150					155				160						165	
atg	gtt	ctt	ggg	gcc	caa	cgc	gaa	aac	ctc	acc	ggg	gca	gcg	gtt	cta	643
Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val	Leu	
				170				175						180		
tac	cgc	tcg	aca	gat	ctt	gaa	aac	tgg	gaa	ttc	tcc	ggg	gaa	atc	acc	691
Tyr	Arg	Ser	Thr	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu	Ile	Thr	
			185				190						195			
ttt	gac	ctc	agt	gat	gca	caa	cct	ggg	tct	gct	cct	gat	ctc	gtt	ccc	739
Phe	Asp	Leu	Ser	Asp	Ala	Gln	Pro	Gly	Ser	Ala	Pro	Asp	Leu	Val	Pro	
		200					205					210				
ggg	ggc	tac	atg	tgg	gaa	tgc	ccc	aac	ctt	ttt	acg	ctt	cgc	gat	gaa	787
Gly	Gly	Tyr	Met	Trp	Glu	Cys	Pro	Asn	Leu	Phe	Thr	Leu	Arg	Asp	Glu	
	215					220					225					
gaa	act	ggc	gaa	gat	ctc	gac	gtg	ctg	att	ttc	tgt	cca	caa	gga	ttg	835
Glu	Thr	Gly	Glu	Asp	Leu	Asp	Val	Leu	Ile	Phe	Cys	Pro	Gln	Gly	Leu	
230					235				240						245	
gac	cga	atc	cac	gat	gag	gtt	act	cac	tac	gca	agc	tct	gac	cag	tgc	883
Asp	Arg	Ile	His	Asp	Glu	Val	Thr	His	Tyr	Ala	Ser	Ser	Asp	Gln	Cys	
				250				255						260		
gga	tat	gtc	gtc	ggc	aag	ctt	gaa	gga	acg	acc	ttc	cgc	gtc	ttg	cga	931
Gly	Tyr	Val	Val	Gly	Lys	Leu	Glu	Gly	Thr	Thr	Phe	Arg	Val	Leu	Arg	
			265					270					275			
gga	ttc	agc	gag	ctg	gat	ttc	ggc	cat	gaa	ttc	tac	gca	ccg	cag	gtt	979
Gly	Phe	Ser	Glu	Leu	Asp	Phe	Gly	His	Glu	Phe	Tyr	Ala	Pro	Gln	Val	
		280				285						290				
gca	gta	aac	ggg	tct	gat	gcc	tgg	ctc	gtg	ggc	tgg	atg	ggg	ctg	ccc	1027
Ala	Val	Asn	Gly	Ser	Asp	Ala	Trp	Leu	Val	Gly	Trp	Met	Gly	Leu	Pro	
		295				300					305					
gcg	cag	gat	gat	cac	cca	aca	gtt	gca	cgg	gaa	gga	tgg	gtg	cac	tgc	1075
Ala	Gln	Asp	Asp	His	Pro	Thr	Val	Ala	Arg	Glu	Gly	Trp	Val	His	Cys	
310					315					320					325	
ctg	act	gtg	ccc	cgc	aag	ctt	cat	ttg	cgc	aac	cac	gcg	atc	tat	caa	1123
Leu	Thr	Val	Pro	Arg	Lys	Leu	His	Leu	Arg	Asn	His	Ala	Ile	Tyr	Gln	
				330				335						340		
gag	ctt	ctt	ctc	cca	gag	ggg	gag	tca	ggg	gta	atc	aga	tct	gta	tta	1171
Glu	Leu	Leu	Leu	Pro	Glu	Gly	Glu	Ser	Gly	Val	Ile	Arg	Ser	Val	Leu	
			345					350					355			

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ggt tct gaa cct gtc cga gta gac atc cga ggc aat att tcc ctc gag 1219
 Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly Asn Ile Ser Leu Glu
 360 365 370

tgg gat ggt gtc cgt ttg tct gtg gat cgt ggt ggt gat cgt cgc gta 1267
 Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly Gly Asp Arg Arg Val
 375 380 385

gct gag gta aaa cct ggc gaa tta gtg atc gcg gac gat aat aca gcc 1315
 Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala Asp Asp Asn Thr Ala
 390 395 400 405

att gag ata act gca ggt gat gga cag 1342
 Ile Glu Ile Thr Ala Gly Asp Gly Gln
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<210> 348

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro
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 20 25 30

Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro
 35 40 45

Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln
 50 55 60

Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser
 65 70 75 80

Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly
 85 90 95

Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg
 100 105 110

Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met
 115 120 125

Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro
 130 135 140

Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp
 145 150 155 160

Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr
 165 170 175

Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe
 180 185 190

Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala

00602740-062300

195 200 205
 Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe
 210 215 220
 Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe
 225 230 235 240
 Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val Thr His Tyr Ala
 245 250 255
 Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr
 260 265 270
 Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe
 275 280 285
 Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly
 290 295 300
 Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu
 305 310 315 320
 Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn
 325 330 335
 His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val
 340 345 350
 Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly
 355 360 365
 Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly
 370 375 380
 Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala
 385 390 395 400
 Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp Gly Gln
 405 410

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 <211> 720
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(720)
 <223> RXA02026

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 Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
 1 5 10 15
 ctt att ttt tat aaa ggg aag tat tat gtt tca cat caa tgg ttc cca 96
 Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
 20 25 30

006290"0420960

tta ggc gca gta cat ggc tta aag tat tgg tat aac tac acg agt gat 144
 Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp
 35 40 45

 gac tta ata aac ttt aaa cct gaa ggg cca ata tta aat cca gat act 192
 Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr
 50 55 60

 aaa tat gac agc cat ggt gtt tat agc ggt agc gct ttt gaa tat aac 240
 Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn
 65 70 75 80

 ggg cat tta tat tat atg tac aca gga aat cat cga gat aat cat tgg 288
 Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp
 85 90 95

 caa cga cat gcg agt cag atg atc gca cga ttg aaa gaa gac ggt tca 336
 Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser
 100 105 110

 gtt gaa aag ttt cca aag cca gta att agc cag caa cca gaa gga tat 384
 Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr
 115 120 125

 aca agt cat ttt aga gat cct aaa gtt ttt aaa tat ggt gag aaa tat 432
 Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr
 130 135 140

 tat gca atc att ggc gca caa aat aat gat cag caa ggt cga tta tta 480
 Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu
 145 150 155 160

 ctt tat aat act gaa gat ata att aat tgg cat tat tta ggt gaa ata 528
 Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile
 165 170 175

 aat aca gag tta gat gat ttt gga tat atg tgg gaa tgc cca gat tac 576
 Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr
 180 185 190

 ttt aat tta gat aat caa gat gtc ata ctt att tgt cca caa ggt att 624
 Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile
 195 200 205

 gaa cca aaa ggc aat cag ttc aaa aat att tat caa agt ggt tat ata 672
 Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile
 210 215 220

 ctt gga aag ttt gat att gaa aag tta aca tat gaa cat gaa aat ttt 720
 Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe
 225 230 235 240

<210> 350

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
 1 5 10 15

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<210> 351
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1594)  
<223> RXA02061
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												1				5	
ggg	tat	cac	cga	cca	gag	ctg	cac	atc	acc	gct	gaa	agt	ggg	gtt	ttg		163
Gly	Tyr	His	Arg	Pro	Glu	Leu	His	Ile	Thr	Ala	Glu	Ser	Gly	Val	Leu		
				10					15						20		
ttt	gca	cct	gca	ggc	gtt	ctg	ttg	gat	gac	gac	acg	tgg	cat	ttc	ttc		211
Phe	Ala	Pro	Ala	Gly	Val	Leu	Leu	Asp	Asp	Asp	Thr	Trp	His	Phe	Phe		
			25					30					35				
cac	cag	tac	cgt	ccc	tca	cca	gat	cac	ggc	ccc	agg	tgg	gcg	cac	caa		259
His	Gln	Tyr	Arg	Pro	Ser	Pro	Asp	His	Gly	Pro	Arg	Trp	Ala	His	Gln		
		40					45				50						
ttc	gca	gag	cgc	act	cca	ttt	gtg	tgg	gat	atc	tgc	gat	gac	gtg	cta		307
Phe	Ala	Glu	Arg	Thr	Pro	Phe	Val	Trp	Asp	Ile	Cys	Asp	Asp	Val	Leu		
	55					60					65						
gcc	cct	gaa	ggc	gat	gaa	acc	cag	gtt	cgc	gct	ggc	tca	gtg	gtg	tcc		355
Ala	Pro	Glu	Gly	Asp	Glu	Thr	Gln	Val	Arg	Ala	Gly	Ser	Val	Val	Ser		
	70				75				80						85		
aac	aac	ggg	ggc	gtt	gat	ctg	tac	ttc	acc	tcg	gtt	gtt	ggc	ccc	act		403
Asn	Asn	Gly	Gly	Val	Asp	Leu	Tyr	Phe	Thr	Ser	Val	Val	Gly	Pro	Thr		
				90					95					100			
tcc	act	atc	cag	ttg	gca	cac	atc	aac	aac	atc	cgt	ggc	acc	acc	gaa		451
Ser	Thr	Ile	Gln	Leu	Ala	His	Ile	Asn	Asn	Ile	Arg	Gly	Thr	Thr	Glu		
			105					110					115				
ctg	atc	aat	gag	gac	gag	ctg	ggg	ctc	gat	cca	gat	gtc	tcc	cga	atc		499
Leu	Ile	Asn	Glu	Asp	Glu	Leu	Gly	Leu	Asp	Pro	Asp	Val	Ser	Arg	Ile		
		120					125					130					
ggc	gaa	gtg	gtt	ggc	aac	act	gat	ggg	tat	gta	aag	ttc	cgc	tca	ccg		547
Gly	Glu	Val	Val	Gly	Asn	Thr	Asp	Gly	Tyr	Val	Lys	Phe	Arg	Ser	Pro		
	135				140					145							
tgc	gtt	atc	cca	ggg	tgg	gaa	gac	caa	gga	aac	cgc	gat	gaa	ggc	cac		595
Cys	Val	Ile	Pro	Gly	Trp	Glu	Asp	Gln	Gly	Asn	Arg	Asp	Glu	Gly	His		
	150				155				160						165		
tca	gga	tgg	ttg	atg	ctc	gca	gtt	act	ggc	cca	gtt	gaa	gcc	cca	aca		643
Ser	Gly	Trp	Leu	Met	Leu	Ala	Val	Thr	Gly	Pro	Val	Glu	Ala	Pro	Thr		
				170					175					180			
gta	gtg	gtc	ctc	gac	tcg	cca	gat	gga	aga	gaa	tgg	tcc	att	aca	ggg		691
Val	Val	Val	Leu	Asp	Ser	Pro	Asp	Gly	Arg	Glu	Trp	Ser	Ile	Thr	Gly		
			185					190					195				
ccc	ctg	tct	ctc	aac	ggc	ctc	tct	gga	tta	gag	tca	gac	gaa	gtt	cta		739
Pro	Leu	Ser	Leu	Asn	Gly	Leu	Ser	Gly	Leu	Glu	Ser	Asp	Glu	Val	Leu		
		200					205					210					
gtt	gct	cct	cgc	atg	att	cgt	ctg	cgc	gat	gaa	gtg	gat	cat	gaa	atc		787
Val	Ala	Pro	Arg	Met	Ile	Arg	Leu	Arg	Asp	Glu	Val	Asp	His	Glu	Ile		
	215					220				225							
tac	gat	gtc	ctc	att	gtc	acc	att	gaa	caa	gac	ggg	att	gac	att	tcg		835
Tyr	Asp	Val	Leu	Ile	Val	Thr	Ile	Glu	Gln	Asp	Gly	Ile	Asp	Ile	Ser		

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230	235	240	245	
gga tac ctg gta ggc cag ctc aac ggc tca gaa ttc gat gtg aag act 883 Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu Phe Asp Val Lys Thr 250 255 260				
cca ttt acc cgc atc gat ttt ggc cat gat ttc tct cgc ccc cgc aac 931 Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe Ser Arg Pro Arg Asn 265 270 275				
acc aac tac gcc gaa acc acc atc ggc tac gac ttc gcc cac atc ttt 979 Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp Phe Ala His Ile Phe 280 285 290				
ggt ctc atg aat ggc gta ggt cgt ttg gac tcc ccc act gag cat ctc 1027 Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser Pro Thr Glu His Leu 295 300 305				
agt tgg aag gaa gaa ggc tgg gca aac gct att tct ttc cca cgt att 1075 Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile Ser Phe Pro Arg Ile 310 315 320 325				
gtc acg ctc cag gac ggt acg gtc ttc cag acc cct cca gaa gga ttg 1123 Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr Pro Pro Glu Gly Leu 330 335 340				
ctt gat gcc att cat gaa tcc gag gca gcg gca ggt tgg acc gga ctg 1171 Leu Asp Ala Ile His Glu Ser Glu Ala Ala Ala Gly Trp Thr Gly Leu 345 350 355				
tgc gaa atc cca tca aac agc gca gtt gaa gtg gcg ttg aag gac caa 1219 Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val Ala Leu Lys Asp Gln 360 365 370				
gaa ggt gaa atc gct gca aca atc act cac cgc cac aat cag cta gtc 1267 Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg His Asn Gln Leu Val 375 380 385				
gtt gat cgg tcc atg aac ccc aac cac gcg ggt gat cca cac gcg att 1315 Val Asp Arg Ser Met Asn Pro Asn His Ala Gly Asp Pro His Ala Ile 390 395 400 405				
gca cca ttg act gat gat gaa aca gat tca ctg ttc att gtc gtt gac 1363 Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu Phe Ile Val Val Asp 410 415 420				
ggc tct aca gta gaa gtt ttt gct gat ggc ggt tat gta tca atg gca 1411 Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly Tyr Val Ser Met Ala 425 430 435				
agc cgt gtg tat ttc aac aac gga cca ttc agc gaa ttt gag gtc acc 1459 Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser Glu Phe Glu Val Thr 440 445 450				
acc acc ggt gac gca agc att att cgc cag gaa agt cac ttc cct gtt 1507 Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu Ser His Phe Pro Val 455 460 465				
gat ttc agt tcg gtg tcc cta gat ata gat gat ctc act gcg ctc atg 1555 Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp Leu Thr Ala Leu Met 470 475 480 485				

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cag ttc gat gaa aac gaa ccg cat gaa ggc cca gtg aga taagagttag 1604
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<211> 498

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

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 20 25 30

Thr Trp His Phe Phe His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro
 35 40 45

Arg Trp Ala His Gln Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile
 50 55 60

Cys Asp Asp Val Leu Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala
 65 70 75 80

Gly Ser Val Val Ser Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser
 85 90 95

Val Val Gly Pro Thr Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile
 100 105 110

Arg Gly Thr Thr Glu Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro
 115 120 125

Asp Val Ser Arg Ile Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val
 130 135 140

Lys Phe Arg Ser Pro Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn
 145 150 155 160

Arg Asp Glu Gly His Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro
 165 170 175

Val Glu Ala Pro Thr Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu
 180 185 190

Trp Ser Ile Thr Gly Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu
 195 200 205

Ser Asp Glu Val Leu Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu
 210 215 220

Val Asp His Glu Ile Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp
 225 230 235 240

Gly Ile Asp Ile Ser Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu
 245 250 255

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ctgcgacgga cctagcaaag gggcgctgac acaagcactg cgtttgctgg tgcgcggaca																60
gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa																115
Met Glu Leu Leu Glu																5
1																
ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat	163															
Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp	20															
10 15																
ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg	211															
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp	35															
25 30																
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Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu	50															
40 45																
aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt	307															
Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val	65															
55 60																
gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca	355															
Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala	85															
70 75 80																
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Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala	100															
90 95																
cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca	451															
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala	115															
105 110 115																
ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt	499															
Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val	130															
120 125 130																
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Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn	145															
135 140 145																
acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac	595															
Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr	165															
150 155 160																
cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg	643															
Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu	180															
170 175 180																
ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc	691															
Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile	195															
185 190 195																
gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt	739															
Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg	210															
200 205 210																
gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa	787															
Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu	225															
215 220 225																

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 Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu Asn Phe
 230 235 240 245

 tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca aac ctt 883
 Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala Asn Leu
 250 255 260

 cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac tcc gac 931
 His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn Ser Asp
 265 270 275

 aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc ccg gag 979
 Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val Pro Glu
 280 285 290

 ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc gtg gac 1027
 Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg Val Asp
 295 300 305

 gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc aac gaa 1075
 Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile Asn Glu
 310 315 320 325

 ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc aac cac 1123
 Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala Asn His
 330 335 340

 gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc ttg gaa 1171
 Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser Leu Glu
 345 350 355

 gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca tgg gtt 1219
 Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala Trp Val
 360 365 370

 cca gca aac gac cca acc att gcg atg cgt tct gag gac gca gaa gta 1267
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<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

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 20 25 30

Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile
 35 40 45

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Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala
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 65 70 75 80
 Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro
 85 90 95
 Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly
 100 105 110
 Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys
 115 120 125
 Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe
 130 135 140
 Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu
 145 150 155 160
 Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu
 165 170 175
 Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys
 180 185 190
 Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu
 195 200 205
 Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile
 210 215 220
 Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala
 225 230 235 240
 Leu Leu Leu Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu
 245 250 255
 Asp Ala Ala Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile
 260 265 270
 Met Ala Asn Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr
 275 280 285
 Val Asp Val Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu
 290 295 300
 Asn Ala Arg Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro
 305 310 315 320
 Val Pro Ile Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu
 325 330 335
 Ala Glu Ala Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly
 340 345 350
 Thr Val Ser Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly
 355 360 365
 His Ala Ala Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser

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370

375

380

Glu Asp Ala Glu Val Phe Leu Ala Arg Val
385 390

<210> 355

<211> 524

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> FRXA01369

<400> 355

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aac ttc tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca	96
Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala	
20 25 30	
aac ctt cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac	144
Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn	
35 40 45	
tcc gac aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc	192
Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val	
50 55 60	
ccg gag ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc	240
Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg	
65 70 75 80	
gtg gac gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc	288
Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile	
85 90 95	
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Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala	
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Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser	
115 120 125	
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Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala	
130 135 140	
tgg gtt cca gca aac gac cca acc att gcg atg cgt tct gag gac gca	480
Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala	
145 150 155 160	
gaa gta ttc ctc gct agg gtt tagatctttt tagattaa tca	524
Glu Val Phe Leu Ala Arg Val	
165	

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